

SEQUENCE LISTING

<110> Gallatin, Michael W.
Van der Vieren, Monica

<120> Novel Human B2

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<150> 08/362,652
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DRAFT - 06/26/04

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His Val Gln Lys Ser Thr Arg Asp Arg Leu Arg Glu Gly Gln Ile Gln
660 665 670

Ser Val Val Thr Tyr Asp Leu Ala Leu Asp Ser Gly Arg Pro His Ser
675 680 685

Arg Ala Val Phe Asn Glu Thr Lys Asn Ser Thr Arg Arg Gln Thr Gln
690 695 700

Val Leu Gly Leu Thr Gln Thr Cys Glu Thr Leu Lys Leu Gln Leu Pro
705 710 715 720

Asn Cys Ile Glu Asp Pro Val Ser Pro Ile Val Leu Arg Leu Asn Phe
725 730 735

Ser Leu Val Gly Thr Pro Leu Ser Ala Phe Gly Asn Leu Arg Pro Val
740 745 750

Leu Ala Glu Asp Ala Gln Arg Leu Phe Thr Ala Leu Phe Pro Phe Glu
755 760 765

Lys Asn Cys Gly Asn Asp Asn Ile Cys Gln Asp Asp Leu Ser Ile Thr
770 775 780

Phe Ser Phe Met Ser Leu Asp Cys Leu Val Val Gly Gly Pro Arg Glu
785 790 795 800

Phe Asn Val Thr Val Thr Val Arg Asn Asp Gly Glu Asp Ser Tyr Arg
805 810 815

Thr Gln Val Thr Phe Phe Pro Leu Asp Leu Ser Tyr Arg Lys Val
820 825 830

Ser Thr Leu Gln Asn Gln Arg Ser Gln Arg Ser Trp Arg Leu Ala Cys
835 840 845

Glu Ser Ala Ser Ser Thr Glu Val Ser Gly Ala Leu Lys Ser Thr Ser
850 855 860

Cys Ser Ile Asn His Pro Ile Phe Pro Glu Asn Ser Glu Val Thr Phe
865 870 875 880

Asn Ile Thr Phe Asp Val Asp Ser Lys Ala Ser Leu Gly Asn Lys Leu
885 890 895

Leu Leu Lys Ala Asn Val Thr Ser Glu Asn Asn Met Pro Arg Thr Asn
900 905 910

Lys Thr Glu Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
915 920 925

Val Val Thr Ser His Gly Val Ser Thr Lys Tyr Leu Asn Phe Thr Ala
930 935 940

Ser Glu Asn Thr Ser Arg Val Met Gln His Gln Tyr Gln Val Ser Asn
945 950 955 960

Leu Gly Gln Arg Ser Leu Pro Ile Ser Leu Val Phe Leu Val Pro Val
965 970 975

Arg Leu Asn Gln Thr Val Ile Trp Asp Arg Pro Gln Val Thr Phe Ser
980 985 990

Glu Asn Leu Ser Ser Thr Cys His Thr Lys Glu Arg Leu Pro Ser His
995 1000 1005

Ser Asp Phe Leu Ala Glu Leu Arg Lys Ala Pro Val Val Asn Cys Ser
1010 1015 1020

Ile Ala Val Cys Gln Arg Ile Gln Cys Asp Ile Pro Phe Phe Gly Ile
1025 1030 1035 1040

Gln Glu Glu Phe Asn Ala Thr Leu Lys Gly Asn Leu Ser Phe Asp Trp
1045 1050 1055

Tyr Ile Lys Thr Ser His Asn His Leu Leu Ile Val Ser Thr Ala Glu
1060 1065 1070

Ile Leu Phe Asn Asp Ser Val Phe Thr Leu Leu Pro Gly Gln Gly Ala
1075 1080 1085

Phe Val Arg Ser Gln Thr Glu Thr Lys Val Glu Pro Phe Glu Val Pro
1090 1095 1100

Asn Pro Leu Pro Leu Ile Val Gly Ser Ser Val Gly Gly Leu Leu Leu
1105 1110 1115 1120

Leu Ala Leu Ile Thr Ala Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg
1125 1130 1135

Gln Tyr Lys Asp Met Met Ser Glu Gly Gly Pro Pro Gly Ala Glu Pro
1140 1145 1150

Gln

<210> 4
<211> 1163
<212> PRT
<213> Homo sapiens

<400> 4
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Ser Leu Gly Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Arg Val
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Asp Ser Ala Gly Phe Gly Asp Ser Val Val Gln Tyr Ala Asn Ser Trp
35 40 45

Val Val Val Gly Ala Pro Gln Lys Ile Ile Ala Ala Asn Gln Ile Gly
50 55 60

Gly Leu Tyr Gln Cys Gly Tyr Ser Thr Gly Ala Cys Glu Pro Ile Gly
65 70 75 80

Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85 90 95

Ala Ser Thr Thr Ser Pro Ser Gln Leu Leu Ala Cys Gly Pro Thr Val
100 105 110

His His Glu Cys Gly Arg Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu
115 120 125

Leu Gly Pro Thr Gln Leu Thr Gln Arg Leu Pro Val Ser Arg Gln Glu
130 135 140

Cys Pro Arg Gln Glu Gln Asp Ile Val Phe Leu Ile Asp Gly Ser Gly
145 150 155 160

Ser Ile Ser Ser Arg Asn Phe Ala Thr Met Met Asn Phe Val Arg Ala
165 170 175

Val Ile Ser Gln Phe Gln Arg Pro Ser Thr Gln Phe Ser Leu Met Gln
180 185 190

Phe Ser Asn Lys Phe Gln Thr His Phe Thr Phe Glu Glu Phe Arg Arg
195 200 205

Thr Ser Asn Pro Leu Ser Leu Leu Ala Ser Val His Gln Leu Gln Gly
210 215 220

Phe Thr Tyr Thr Ala Thr Ala Ile Gln Asn Val Val His Arg Leu Phe
225 230 235 240

His Ala Ser Tyr Gly Ala Arg Arg Asp Ala Ile Lys Ile Leu Ile Val
245 250 255

Ile Thr Asp Gly Lys Lys Glu Gly Asp Ser Leu Asp Tyr Lys Asp Val
260 265 270

Ile Pro Met Ala Asp Ala Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val
275 280 285

Gly Leu Ala Phe Gln Asn Arg Asn Ser Trp Lys Glu Leu Asn Asp Ile
290 295 300

Ala Ser Lys Pro Ser Gln Glu His Ile Phe Lys Val Glu Asp Phe Asp
305 310 315 320

Ala Leu Lys Asp Ile Gln Asn Gln Leu Lys Glu Lys Ile Phe Ala Ile
325 330 335

Glu Gly Thr Glu Thr Ile Ser Ser Ser Phe Glu Leu Glu Met Ala
340 345 350

Gln Glu Gly Phe Ser Ala Val Phe Thr Pro Asp Gly Pro Val Leu Gly
355 360 365

Ala Val Gly Ser Phe Thr Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro
370 375 380

Asn Met Ser Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met
385 390 395 400

Arg Asp Ser Tyr Leu Gly Tyr Ser Thr Glu Leu Ala Leu Trp Lys Gly
405 410 415

Val Gln Ser Leu Val Leu Gly Ala Pro Arg Tyr Gln His Ile Gly Lys
420 425 430

Ala Val Ile Phe Ile Gln Val Ser Arg Gln Trp Arg Met Lys Ala Glu
435 440 445

Val Ile Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser
450 455 460

Val Asp Val Asp Thr Asp Gly Ser Thr Asp Leu Val Leu Ile Gly Ala
465 470 475 480

Pro His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Cys Pro
485 490 495

Leu Pro Arg Gly Trp Arg Arg Trp Trp Cys Asp Ala Val Leu Tyr Gly
500 505 510

Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu
515 520 525

Gly Asp Val Asn Gly Asp Lys Leu Thr Asp Val Val Ile Gly Ala Pro
530 535 540

Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Leu Phe His Gly Val Leu
545 550 555 560

Gly Pro Ser Ile Ser Pro Ser His Ser Gln Arg Ile Ala Gly Ser Gln
565 570 575

Leu Ser Ser Arg Leu Gln Tyr Phe Gly Gln Ala Leu Ser Gly Gly Gln
580 585 590

Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Arg Gly
595 600 605

Gln Val Leu Leu Leu Arg Thr Arg Pro Val Leu Trp Val Gly Val Ser
610 615 620

Met Gln Phe Ile Pro Ala Glu Ile Pro Arg Ser Ala Phe Glu Cys Arg
625 630 635 640

Glu Gln Val Val Ser Glu Gln Thr Leu Val Gln Ser Asn Ile Cys Leu
645 650 655

Tyr Ile Asp Lys Arg Ser Lys Asn Leu Leu Gly Ser Arg Asp Leu Gln
660 665 670

Ser Ser Val Thr Leu Asp Leu Ala Leu Ala Pro Gly Arg Leu Ser Pro
675 680 685

Arg Ala Ile Phe Gln Glu Thr Lys Asn Arg Ser Leu Ser Arg Val Arg
690 695 700

Val Leu Gly Leu Lys Ala His Cys Glu Asn Phe Asn Leu Leu Leu Pro
705 710 715 720

Ser Cys Val Glu Asp Ser Val Ile Pro Ile Ile Leu Arg Leu Asn Phe
725 730 735

Thr Leu Val Gly Lys Pro Leu Leu Ala Phe Arg Asn Leu Arg Pro Met
740 745 750

Leu Ala Ala Leu Ala Gln Arg Tyr Phe Thr Ala Ser Leu Pro Phe Glu
755 760 765

Lys Asn Cys Gly Ala Asp His Ile Cys Gln Asp Asn Leu Gly Ile Ser
770 775 780

Phe Ser Phe Pro Gly Leu Lys Ser Leu Leu Val Gly Ser Asn Leu Glu
785 790 795 800

Leu Asn Ala Glu Val Met Val Trp Asn Asp Gly Glu Asp Ser Tyr Gly
805 810 815

Thr Thr Ile Thr Phe Ser His Pro Ala Gly Leu Ser Tyr Arg Tyr Val
820 825 830

Ala Glu Gly Gln Lys Gln Gly Gln Leu Arg Ser Leu His Leu Thr Cys
835 840 845

Cys Ser Ala Pro Val Gly Ser Gln Gly Thr Trp Ser Thr Ser Cys Arg
850 855 860

Ile Asn His Leu Ile Phe Arg Gly Ala Gln Ile Thr Phe Leu Ala
865 870 875 880

Thr Phe Asp Val Ser Pro Lys Ala Val Gly Leu Asp Arg Leu Leu Leu
885 890 895

Ile Ala Asn Val Ser Ser Glu Asn Asn Ile Pro Arg Thr Ser Lys Thr
900 905 910

Ile Phe Gln Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Ile Val Val
915 920 925

Ser Ser His Glu Gln Phe Thr Lys Tyr Leu Asn Phe Ser Glu Ser Glu
930 935 940

Glu Lys Glu Ser His Val Ala Met His Arg Tyr Gln Val Asn Asn Leu
945 950 955 960

Gly Gln Arg Asp Leu Pro Val Ser Ile Asn Phe Trp Val Pro Val Glu
965 970 975

Leu Asn Gln Glu Ala Val Trp Met Asp Val Glu Val Ser His Pro Gln
980 985 990

Asn Pro Ser Leu Arg Cys Ser Ser Glu Lys Ile Ala Pro Pro Ala Ser
995 1000 1005

Asp Phe Leu Ala His Ile Gln Lys Asn Pro Val Leu Asp Cys Ser Ile
1010 1015 1020

Ala Gly Cys Leu Arg Phe Arg Cys Asp Val Pro Ser Phe Ser Val Gln
1025 1030 1035 1040

Glu Glu Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe Gly Trp Val
1045 1050 1055

Arg Gln Ile Leu Gln Lys Lys Val Ser Val Val Ser Val Ala Glu Ile
1060 1065 1070

Ile Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe
1075 1080 1085

Met Arg Ala Gln Thr Ile Thr Val Leu Glu Lys Tyr Lys Val His Asn
1090 1095 1100

Pro Ile Pro Leu Ile Val Gly Ser Ser Ile Gly Gly Leu Leu Leu
1105 1110 1115 1120

Ala Leu Ile Thr Ala Val Leu Tyr Lys Val Gly Phe Phe Lys Arg Gln
1125 1130 1135

Tyr Lys Glu Met Met Glu Glu Ala Asn Gly Gln Ile Ala Pro Glu Asn
1140 1145 1150

Gly Thr Gln Thr Pro Ser Pro Pro Ser Glu Lys
1155 1160

<210> 5
<211> 12
<212> PRT
<213> dog

<400> 5
Phe Asn Leu Asp Val Glu Glu Pro Met Val Phe Gln
1 5 10

<210> 6
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6
ttyaayytgg aytngarga rccnatggtn ttyca

35

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
ttcaacctgg acgtggagga gcccattggtg ttccaa

36

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
ttcaacctgg acgtngaasa ncccatggtc ttccaa

36

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
ttyaayytng aytngarga rcc

23

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
ttyaayytgg acgtngaaga

20

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
tgraanacca tnggytc 17

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
ttggaagacc atnggytc 18

<210> 13
<211> 17
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 13
attaaaccctc actaaag 17

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
ataacgactc actatag 17

<210> 15
<211> 11
<212> PRT
<213> dog

<400> 15
Val Phe Gln Glu Xaa Gly Ala Gly Phe Gly Gln
1 5 10

<210> 16
<211> 14
<212> PRT
<213> dog

<400> 16
Leu Tyr Asp Xaa Val Ala Ala Thr Gly Leu Xaa Gln Pro Ile
1 5 10

<210> 17
<211> 12

<212> PRT
<213> dog

<400> 17
Pro Leu Glu Tyr Xaa Asp Val Ile Pro Gln Ala Glu
1 5 10

<210> 18
<211> 10
<212> PRT
<213> dog

<400> 18
Phe Gln Glu Gly Phe Ser Xaa Val Leu Xaa
1 5 10

<210> 19
<211> 14
<212> PRT
<213> dog

<400> 19
Thr Ser Pro Thr Phe Ile Xaa Met Ser Gln Glu Asn Val Asp
1 5 10

<210> 20
<211> 17
<212> PRT
<213> dog

<400> 20
Leu Val Val Gly Ala Pro Leu Glu Val Val Ala Val Xaa Gln Thr Gly
1 5 10 15

Arg

<210> 21
<211> 9
<212> PRT
<213> dog

<400> 21
Leu Asp Xaa Lys Pro Xaa Asp Thr Ala
1 5

<210> 22
<211> 7
<212> PRT
<213> dog

<400> 22
Phe Gly Glu Gln Phe Ser Glu
1 5

<210> 23

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
raanccytcy tgraaactyt c

21

<210> 24
<211> 1006
<212> DNA
<213> dog

<400> 24
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gcgtggccca gcttggcgga tctagactcg tgggtggagc cccccctggag gtgggtggcg 120
tcaaccacaaac aggaagggtt tattactgtg tggctgccac tggccttgc aaccctatacc 180
cctgcacacaca ccccccagatg ctgtgaacat gtcctgggt ctgtccctgt cagccgccc 240
cagtcgcccc tggctgctgg cctgtggccc aaccatgcac agagctgtg gggagaatat 300
gtatgcagaa ggctttgcc tcctgttgg a ctcctatctg cagaccattt ggacagtacc 360
tgctgcccta ccagagtgtc caagtcaaga gatggacatt gtcttcctga ttgatggttc 420
tggcagtatg agcaaagtga cttaaacaat atgaaggatt tgtgagagct gtgatgggac 480
agtttgaggg cacccaaacc ctgttctcac tgatacagta tcccacctcc ctgaagatcc 540
acttcaccc t caccatc cagagcagct ggaaccctct gagcctggc gatcccattt 600
tccaactggc cggcctgaca tatacagcca cgggcattcc gaaagtggc gaggaactgt 660
ttcatagtaa gaatggggcc cgtaaaagtgc ccaagaagat cctcattgtc atcacagatg 720
gcaaaaatac aaagacccccc tggagtacga ggacgtatcc ccaggcagag agagcggatc 780
atccgctatg ccattgggtt gggagatgct ttctggaaac ccagtgcac gcaggagctg 840
gacaacattt gctcagagcc ggctcaggac catgtgttca gggtggacaa ctttgcac 900
ctcagcagca tccaggagca gctgcaggag aagatctttt cactcgaagg aaccctgtc 960
acgacaagta gctcttcca acatgagatg ttccaagaag gttca 1006

<210> 25
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 25
gtnttgcarg argaygg

17

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
ccactgtcaag gatgcccgtg 20

<210> 27
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 27
agttacgaat tcgccaccat ggctctacgg gtgcttcttc tg 42

<210> 28
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
agttacgaat tcgccaccat gactcggact gtgcttcttc tg 42

<210> 29
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
agttacgaat tcgccaccat gaccttcggc actgtg 36

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
tttgctgactg cctgcagttc 20

<210> 31

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gttctgacgc gtaatggcat tgttagacctc gtcttc 36

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
acgtatgcag gatcccatca agagatggac atcgct 36

<210> 33
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
actgcattgtc tcgaggctga agccttcttg ggacatc 37

<210> 34
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
tatagactgc tggtagtcc ccac 24

<210> 35
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
tgaagattgg gggtaataaa caga 24

<210> 36
<211> 3528
<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (1)..(3453)

<220>

<223> Description of Artificial Sequence: primer

<400> 36

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Gly Trp Ala Leu Ala Ser Cys His Gly Ser Asn Leu Asp Val Glu Glu	
1 5 10 15	

ccc atc gtg ttc aga gag gat gca gcc agc ttt gga cag act gtg gtg	96
Pro Ile Val Phe Arg Glu Asp Ala Ala Ser Phe Gly Gln Thr Val Val	
20 25 30	

cag ttt ggt gga tct cga ctc gtg gtg gga gcc cct ctg gag gcg gtg	144
Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala Pro Ile Glu Ala Val	
35 40 45	

gca gtc aac caa aca gga cgg ttg tat gac ttt gca cct gcc act ggc	192
Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly	
50 55 60	

atg tgc cag ccc atc gta ctg cgc agt ccc cta gag gca gtg aac atg	240
Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu Glu Ala Val Asn Met	
65 70 75 80	

tcc ctg ggc ctg tct ctg gtg act gcc acc aat aac gcc cag ttg ctg	288
Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn Asn Ala Gln Leu Leu	
85 90 95	

gct tgt ggt cca act gca cag aga gct tgt gtg aag aac atg tat gcg	336
Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val Lys Asn Met Tyr Ala	
100 105 110	

aaa ggt tcc tgc ctc ctt ctc ggc tcc agc ttg cag ttc atc cag gca	384
Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala	
115 120 125	

gtc cct gcc tcc atg cca gag tgt cca aga caa gag atg gac att gct	432
Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln Glu Met Asp Ile Ala	
130 135 140	

ttc ctg att gat ggt tct ggc agc att aac caa agg gac ttt gcc cag	480
Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln	
145 150 155 160	

atg aag gac ttt gtc aaa gct ttg atg gga gag ttt gcg agc acc agc	528
Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu Phe Ala Ser Thr Ser	
165 170 175	

acc ttg ttc tcc ctg atg caa tac tcg aac atc ctg aag acc cat ttt	576
Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile Leu Lys Thr His Phe	
180 185 190	

acc ttc act gaa ttc aag aac atc ctg gac cct cag agc ctg gtg gat	624
Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro Gln Ser Leu Val Asp	
195 200 205	

ccc att gtc cag ctg caa ggc ctg acc tac aca gcc aca ggc atc cgg Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg 210 215 220	672
aca gtg atg gaa gag cta ttt cat agc aag aat ggg tcc cgt aaa agt Thr Val Met Glu Glu Leu Phe His Ser Lys Asn Gly Ser Arg Lys Ser 225 230 235 240	720
gcc aag aag atc ctc ctt gtc atc aca gat ggg cag aaa tac aga gac Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp 245 250 255	768
ccc ctg gag tat agt gat gtc att ccc gcc gca gac aaa gct ggc atc Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala Asp Lys Ala Gly Ile 260 265 270	816
att cgt tat gct att ggg gtg gga gat gcc ttc cag gag ccc act gcc Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe Gln Glu Pro Thr Ala 275 280 285	864
ctg aag gag ctg aac acc att ggc tca gct ccc cca cag gac cac gtg Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro Pro Gln Asp His Val 290 295 300	912
tcc aag gta ggc aac ttt gca gca ctt cgc agc atc cag agg caa ctt Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu 305 310 315 320	960
cag gag aaa atc ttc gcc att gag gga act caa tca agg tca agt agt Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser 325 330 335	1008
tcc ttt cag cac gag atg tca caa gaa ggt ttc agt tca gct ctc aca Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr 340 345 350	1056
tcg gat gga ccc gtt ctg ggg gcc gyg gga agc ttc agc tgg tcc gga Ser Asp Gly Pro Val Leu Gly Ala Xaa Gly Ser Phe Ser Trp Ser Gly 355 360 365	1104
ggt gcc ttc tta tat ccc cca aat acg aga ccc acc ttt atc aac atg Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro Thr Phe Ile Asn Met 370 375 380	1152
tct cag gag aat gtg gac atg aga gac tcc tac ctg ggt tac tcc acc Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr 385 390 395 400	1200
gca gtg gcc ttt tgg aag ggg gtt cac agc ctg atc ctg ggg gcc ccg Ala Val Ala Phe Trp Lys Gly Val His Ser Leu Ile Leu Gly Ala Pro 405 410 415	1248
cgt cac cag cac acg ggg aag gtt gtc atc ttt acc cag gaa gcc agg Arg His Gln His Thr Gly Lys Val Val Ile Phe Thr Gln Glu Ala Arg 420 425 430	1296
cat tgg agg ccc aag tct gaa gtc aga ggg aca cag atc ggc tcc tac His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr 435 440 445	1344

ttc ggg gcc tct ctc tgt tct gtg gac gtg gat aga gat ggc agc acy 1392
Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp Arg Asp Gly Ser Xaa
450 455 460

gac ctg gtc ctg atc gga gcc ccc cat tac tat gag cag acc cga ggg 1440
Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly
465 470 475 480

ggg cag gtc tca gtg tkc ccc gtg ccc ggt gtg agg ggc agg tgg cag 1488
Gly Gln Val Ser Val Xaa Pro Val Pro Gly Val Arg Gly Arg Trp Gln
485 490 495

tgt gag gcc acc ctc cac ggg gag cag grc cat cct tgg ggc cgc ttt 1536
Cys Glu Ala Thr Leu His Gly Glu Gln Xaa His Pro Trp Gly Arg Phe
500 505 510

ggg gtg gct ctg aca gtg ctg ggg gac gta aac ggg gac aat ctg gca 1584
Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn Gly Asp Asn Leu Ala
515 520 525

gac gtg gct att ggt gcc cct gga gag gag gag agc aga ggt gct gtc 1632
Asp Val Ala Ile Gly Ala Pro Gly Glu Glu Ser Arg Gly Ala Val
530 535 540

tac ata ttt cat gga gcc tcg aga ctg gag atc atg ccc tca ccc agc 1680
Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile Met Pro Ser Pro Ser
545 550 555 560

cag cgg gtc act ggc tcc cag ctc tcc ctg aga ctg cag tat ttt ggg 1728
Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly
565 570 575

cag tca ttg agt ggg ggt cag gac ctt aca cag gat ggc ctg gtg gac 1776
Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln Asp Gly Leu Val Asp
580 585 590

ctg gcc gtg gga gcc cag ggg cac gta ctg ctg ctc agg agt ctg cct 1824
Leu Ala Val Gly Ala Gln Gly His Val Leu Leu Leu Arg Ser Leu Pro
595 600 605

ctg ctg aaa gtg gag ctc tcc ata aga ttc gcc ccc atg gag gtg gca 1872
Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala Pro Met Glu Val Ala
610 615 620

aag gct gtg tac cag tgc tgg gaa agg act ccc act gtc ctc gaa gct 1920
Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro Thr Val Leu Glu Ala
625 630 635 640

gga gag gcc act gtc tgt ctc act gtc cac aaa ggc tca cct gac ctg 1968
Gly Glu Ala Thr Val Cys Leu Thr Val His Lys Gly Ser Pro Asp Leu
645 650 655

tta ggt aat gtc caa ggc tct gtc agg tat gat ctg gcg tta gat ccg 2016
Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro
660 665 670

ggc cgc ctg att tct cgt gcc att ttt gat gag act aag aac tgc act 2064
Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr
675 680 685

ttg acg gga agg aag act ctg ggg ctt ggt gat cac tgc gaa aca gtg 2112
Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp His Cys Glu Thr Val
690 695 700

aag ctg ctt ttg ccg gac tgt gtg gaa gat gca gtg agc cct atc atc 2160
Lys Leu Leu Leu Pro Asp Cys Val Glu Asp Ala Val Ser Pro Ile Ile
705 710 715 720

ctg cgc ctc aac ttt tcc ctg gtg aga gac tct gct tca ccc agg aac 2208
Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser Ala Ser Pro Arg Asn
725 730 735

ctg cat cct gtg ctg gct gtg ggc tca caa gac cac ata act gct tct 2256
Leu His Pro Val Leu Ala Val Gly Ser Gln Asp His Ile Thr Ala Ser
740 745 750

ctg ccg ttt gag aag aac tgt aag caa gaa ctc ctg tgt gag ggg gac 2304
Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp
755 760 765

ctg ggc atc agc ttt aac ttc tca ggc ctg cag gtc ttg gtg gtg gga 2352
Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Val Val Gly
770 775 780

ggc tcc cca gag ctc act gtg aca gtc act gtg tgg aat gag ggt gag 2400
Gly Ser Pro Glu Leu Thr Val Thr Val Trp Asn Glu Gly Glu
785 790 795 800

gac agc tat gga act tta gtc aag ttc tac tac cca gca ggg cta tct 2448
Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser
805 810 815

tac cga cgg gta aca ggg act cag caa cct cat cag tac cca cta cgc 2496
Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His Gln Tyr Pro Leu Arg
820 825 830

ttg gcc tgt gag gct gag ccc gct gcc cag gag gac ctg agg agc agc 2544
Leu Ala Cys Glu Ala Glu Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser
835 840 845

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Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr
850 855 860

ttc atg atc aca ttc gat gtc tcc tac aag gcc ttc cta gga gac agg 2640
Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg
865 870 875 880

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Leu Leu Leu Arg Ala Lys Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr
885 890 895

aac aag act gcc ttc cag ctg gag ctc cca gtg aag tac acc gtc tat 2736
Asn Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr
900 905 910

acc ctg atc agt agg caa gaa gat tcc acc aac cat gtc aac ttt tca 2784
Thr Leu Ile Ser Arg Gln Glu Asp Ser Thr Asn His Val Asn Phe Ser
915 920 925

tct tcc cac ggg ggg aga agg caa gaa gcc gca cat cgc tat cgt gtg 2832
Ser Ser His Gly Gly Arg Arg Gln Glu Ala Ala His Arg Tyr Arg Val
930 935 940

aat aac ctg agt cca ctg aag ctg gcc gtc aga gtt aac ttc tgg gtc 2880
Asn Asn Leu Ser Pro Leu Lys Leu Ala Val Arg Val Asn Phe Trp Val
945 950 955 960

cct gtc ctt ctg aac ggt gtg gct gtg tgg gac gtg act ctg agc agc 2928
Pro Val Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu Ser Ser
965 970 975

cca gca cag ggt gtc tcc tgc gtg tcc cag atg aaa cct cct cag aat 2976
Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met Lys Pro Pro Gln Asn
980 985 990

ccc gac ttt ctg acc cag att cag aga cgt tct gtg ctg gac tgc tcc 3024
Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser Val Leu Asp Cys Ser
995 1000 1005

att gct gac tgc ctg cac tcc cgc tgt gac atc ccc tcc ttg gac atc 3072
Ile Ala Asp Cys Leu His Ser Arg Cys Asp Ile Pro Ser Leu Asp Ile
1010 1015 1020

cag gat gaa ctt gac ttc att ctg agg ggc aac ctc agc ttc ggc tgg 3120
Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp
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gtc agt cag aca ttg cag gaa aag gtg ttg ctt gtg agt gag gct gaa 3168
Val Ser Gln Thr Leu Gln Glu Lys Val Leu Leu Val Ser Glu Ala Glu
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atc act ttc gac aca tct gtg tac tcc cag ctg cca gga cag gag gca 3216
Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala
1060 1065 1070

ttt ctg aga gcc cag gtg gag aca acg tta gaa gaa tac gtg gtc tat 3264
Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu Tyr Val Val Tyr
1075 1080 1085

gag ccc atc ttc ctc gtg gcg ggc agc tcg gtg gga ggt ctg ctg tta 3312
Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val Gly Gly Leu Leu Leu
1090 1095 1100

ctg gct ctc atc aca gtg gta ctg tac aag ctt ggc tyc tyc aaa cgt 3360
Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu Gly Xaa Xaa Lys Arg
1105 1110 1115 1120

cag tac aaa gaa atg ctg gac ggc aag gct gca gat cct gtc aca gcc 3408
Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala Asp Pro Val Thr Ala
1125 1130 1135

ggc cag gca gat ttc ggc tgt gag act cct cca tat ctc gtg agc 3453
Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro Tyr Leu Val Ser
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Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala Pro Leu Glu Ala Val
35 40 45

Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly
50 55 60

Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu Glu Ala Val Asn Met
65 70 75 80

Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn Asn Ala Gln Leu Leu
85 90 95

Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val Lys Asn Met Tyr Ala
100 105 110

Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala
115 120 125

Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln Glu Met Asp Ile Ala
130 135 140

Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln
145 150 155 160

Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu Phe Ala Ser Thr Ser
165 170 175

Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile Leu Lys Thr His Phe
180 185 190

Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro Gln Ser Leu Val Asp
195 200 205

Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg
210 215 220

Thr Val Met Glu Glu Leu Phe His Ser Lys Asn Gly Ser Arg Lys Ser
225 230 235 240

Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp
245 250 255

Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala Asp Lys Ala Gly Ile
260 265 270

Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe Gln Glu Pro Thr Ala
275 280 285

Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro Pro Gln Asp His Val
290 295 300

Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu
305 310 315 320

Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser
325 330 335

Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr
340 345 350

Ser Asp Gly Pro Val Leu Gly Ala Xaa Gly Ser Phe Ser Trp Ser Gly
355 360 365

Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro Thr Phe Ile Asn Met
370 375 380

Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr
385 390 395 400

Ala Val Ala Phe Trp Lys Gly Val His Ser Leu Ile Leu Gly Ala Pro
405 410 415

Arg His Gln His Thr Gly Lys Val Val Ile Phe Thr Gln Glu Ala Arg
420 425 430

His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr
435 440 445

Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp Arg Asp Gly Ser Xaa
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Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly
465 470 475 480

Gly Gln Val Ser Val Xaa Pro Val Pro Gly Val Arg Gly Arg Trp Gln
485 490 495

Cys Glu Ala Thr Leu His Gly Glu Gln Xaa His Pro Trp Gly Arg Phe
500 505 510

Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn Gly Asp Asn Leu Ala
515 520 525

Asp Val Ala Ile Gly Ala Pro Gly Glu Glu Ser Arg Gly Ala Val
530 535 540

Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile Met Pro Ser Pro Ser
545 550 555 560

Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly
565 570 575

Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln Asp Gly Leu Val Asp
580 585 590

Leu Ala Val Gly Ala Gln Gly His Val Leu Leu Leu Arg Ser Leu Pro
595 600 605

Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala Pro Met Glu Val Ala
610 615 620

Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro Thr Val Leu Glu Ala
625 630 635 640

Gly Glu Ala Thr Val Cys Leu Thr Val His Lys Gly Ser Pro Asp Leu
645 650 655

Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro
660 665 670

Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr
675 680 685

Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp His Cys Glu Thr Val
690 695 700

Lys Leu Leu Leu Pro Asp Cys Val Glu Asp Ala Val Ser Pro Ile Ile
705 710 715 720

Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser Ala Ser Pro Arg Asn
725 730 735

Leu His Pro Val Leu Ala Val Gly Ser Gln Asp His Ile Thr Ala Ser
740 745 750

Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp
755 760 765

Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Val Val Gly
770 775 780

Gly Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp Asn Glu Gly Glu
785 790 795 800

Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser
805 810 815

Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His Gln Tyr Pro Leu Arg
820 825 830

Leu Ala Cys Glu Ala Glu Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser
835 840 845

Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr
850 855 860

Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg
865 870 875 880

Leu Leu Leu Arg Ala Lys Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr
885 890 895

Asn Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr
900 905 910

Thr Leu Ile Ser Arg Gln Glu Asp Ser Thr Asn His Val Asn Phe Ser
915 920 925

Ser Ser His Gly Gly Arg Arg Gln Glu Ala Ala His Arg Tyr Arg Val
930 935 940

Asn Asn Leu Ser Pro Leu Lys Leu Ala Val Arg Val Asn Phe Trp Val
945 950 955 960

Pro Val Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu Ser Ser
965 970 975

Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met Lys Pro Pro Gln Asn
980 985 990

Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser Val Leu Asp Cys Ser
995 1000 1005

Ile Ala Asp Cys Leu His Ser Arg Cys Asp Ile Pro Ser Leu Asp Ile
1010 1015 1020

Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp
1025 1030 1035 1040

Val Ser Gln Thr Leu Gln Glu Lys Val Leu Leu Val Ser Glu Ala Glu
1045 1050 1055

Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala
1060 1065 1070

Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu Glu Tyr Val Val Tyr
1075 1080 1085

Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val Gly Gly Leu Leu Leu
1090 1095 1100

Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu Gly Xaa Xaa Lys Arg
1105 1110 1115 1120

Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala Asp Pro Val Thr Ala
1125 1130 1135

Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro Tyr Leu Val Ser
1140 1145 1150

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<220>

<223> Description of Artificial Sequence: primer

<400> 38

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<210> 39

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<212> DNA

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23

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<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<400> 41
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<210> 43
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<210> 45
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<220>
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<222> (52)..(3516)

<220>

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Met Val
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Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser Cys His
5 10 15

ggg tct aac ctg gat gtg gag aag ccc gtc gtg ttc aaa gag gat gca 153
Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu Asp Ala
20 25 30

gcc agc ttc gga cag act gtg gtg cag ttt ggt gga tct cga ctc gtg 201
Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Ser Arg Leu Val
35 40 45 50

gtg gga gcc cct ctg gag gcg gtg gca gtc aac caa aca gga cag tcg 249
Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly Gln Ser
55 60 65

tct gac tgt ccg cct gcc act ggc gtg tgc cag ccc atc tta ctg cac 297
Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu Leu His
70 75 80

att ccc cta gag gca gtg aac atg tcc ctg ggc ctg tct ctg gtg gct 345
Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Val Ala
85 90 95

gac acc aat aac tcc cag ttg ctg gct tgt ggt cca act gca cag aga 393
Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala Gln Arg
100 105 110

gct tgt gca aag aac atg tat gca aaa ggt tcc tgc ctc ctt ctg ggc 441
Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu Leu Gly
115 120 125 130

tcc agc ttg cag ttc atc cag gca atc cct gct acc atg cca gag tgt 489
Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro Glu Cys
135 140 145

cca gga caa gag atg gac att gct ttc ctg att gat ggc tcc ggc agc 537
Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser
150 155 160

att gat caa agt gac ttt acc cag atg aag gac ttc gtc aaa gct ttg 585
Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys Ala Leu
165 170 175

atg ggc cag ttg gcg agc acc agc acc tcg ttc tcc ctg atg caa tac 633
Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met Gln Tyr
180 185 190

tca aac atc ctg aag act cat ttt acc ttc acg gaa ttc aag agc agc 681
Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys Ser Ser
195 200 205 210

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Leu	Ser	Pro	Gln	Ser	Leu	Val	Asp	Ala	Ile	Val	Gln	Leu	Gln	Gly	Leu		
215					220										225		
acg	tac	aca	gcc	tcg	ggc	atc	cag	aaa	gtg	gtg	aaa	gag	cta	ttt	cat	777	
Thr	Tyr	Thr	Ala	Ser	Gly	Ile	Gln	Lys	Val	Val	Lys	Glu	Leu	Phe	His		
230					235										240		
agc	aag	aat	ggg	gcc	cga	aaa	agt	gcc	aag	aag	ata	cta	att	gtc	atc	825	
Ser	Lys	Asn	Gly	Ala	Arg	Lys	Ser	Ala	Lys	Lys	Ile	Leu	Ile	Val	Ile		
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Thr	Asp	Gly	Gln	Lys	Phe	Arg	Asp	Pro	Leu	Glu	Tyr	Arg	His	Val	Ile		
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Pro	Glu	Ala	Glu	Lys	Ala	Gly	Ile	Ile	Arg	Tyr	Ala	Ile	Gly	Val	Gly		
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Asp	Ala	Phe	Arg	Glu	Pro	Thr	Ala	Leu	Gln	Glu	Leu	Asn	Thr	Ile	Gly		
295					300										305		
tca	gct	ccc	tcg	cag	gac	cac	gtg	tcc	aag	gtg	ggc	aat	ttt	gta	gca	1017	
Ser	Ala	Pro	Ser	Gln	Asp	His	Val	Phe	Lys	Val	Gly	Asn	Phe	Val	Ala		
310					315										320		
ctt	cgc	agc	atc	cag	cgg	caa	att	cag	gag	aaa	atc	ttt	gcc	att	gaa	1065	
Leu	Arg	Ser	Ile	Gln	Arg	Gln	Ile	Gln	Glu	Lys	Ile	Phe	Ala	Ile	Glu		
325					330						335						
gga	acc	gaa	tca	agg	tca	agt	agt	tcc	ttt	cag	cac	gag	atg	tca	caa	1113	
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340					345						350						
gaa	ggt	ttc	agc	tca	gct	ctc	tca	atg	gat	gga	cca	gtt	ctg	ggg	gct	1161	
Glu	Gly	Phe	Ser	Ser	Ala	Leu	Ser	Met	Asp	Gly	Pro	Val	Leu	Gly	Ala		
355					360						365				370		
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Val	Gly	Gly	Phe	Ser	Trp	Ser	Gly	Gly	Ala	Phe	Leu	Tyr	Pro	Ser	Asn		
375					380						385						
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Met	Arg	Ser	Thr	Phe	Ile	Asn	Met	Ser	Gln	Glu	Asn	Glu	Asp	Met	Arg		
390					395						400						
gac	gct	tac	ctg	ggt	tac	tcc	acc	gca	ctg	gcc	ttt	tgg	aag	ggg	gtc	1305	
Asp	Ala	Tyr	Leu	Gly	Tyr	Ser	Thr	Ala	Leu	Ala	Phe	Trp	Lys	Gly	Val		
405					410						415						
cac	agc	ctg	atc	ctg	ggg	gcc	cct	cgc	cac	cag	cac	acg	ggg	aag	gtt	1353	
His	Ser	Leu	Ile	Leu	Gly	Ala	Pro	Arg	His	Gln	His	Thr	Gly	Lys	Val		
420					425						430						
gtc	atc	ttt	acc	cag	gaa	tcc	agg	cac	tgg	agg	ccc	aag	tct	gaa	gtc	1401	
Val	Ile	Phe	Thr	Gln	Glu	Ser	Arg	His	Trp	Arg	Pro	Lys	Ser	Glu	Val		
435					440						445				450		

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cag ggc cat cct tgg ggc cgc ttt ggg gcg gct ctg aca gtg cta ggg Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val Leu Gly 515 520 525 530	1641
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agg act ccc act gtc ctc gaa gct gga gag gcc acc gtc tgt ctc act Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys Leu Thr 645 650 655	2025
gtc cgc aaa ggt tca cct gac ctg tta ggt gat gtc caa agc tct gtc Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser Ser Val 660 665 670	2073
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gag gat gca gtg acc cct atc atc ctg cgc ctt aac tta tcc ctg gca Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser Leu Ala 725 730 735	2265
ggg gac tct gct cca tcc agg aac ctt cgt cct gtg ctg gct gtg ggc Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala Val Gly 740 745 750	2313
tca caa gac cat gta aca gct tct ttc ccg ttt gag aag aac tgt gag Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn Cys Glu 755 760 765 770	2361
ggg aac ctg ggc gtc agc ttc aac ttc tca ggc ctg cag gtc ttg gag Gly Asn Leu Gly Val Ser Phe Asn Phe Ser Gly Leu Gln Val Leu Glu 775 780 785	2409
gta gga agc tcc cca gag ctc act gtg aca gta aca gtt tgg aat gag Val Gly Ser Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp Asn Glu 790 795 800	2457
gtt gag gac agc tat gga acc tta atc aag ttc tac tac cca gca gag Gly Glu Asp Ser Tyr Gly Thr Leu Ile Lys Phe Tyr Tyr Pro Ala Glu 805 810 815	2505
cta tct tac cga cgg gtg aca aga gcc cag caa cct cat ccg tac cca Leu Ser Tyr Arg Arg Val Thr Arg Ala Gln Gln Pro His Pro Tyr Pro 820 825 830	2553
cta cgc ctg gca tgt gag gct gag ccc acg ggc cag gag agc ctg agg Leu Arg Leu Ala Cys Glu Ala Glu Pro Thr Gly Gln Glu Ser Leu Arg 835 840 845 850	2601
agc agc agc tgt agc atc aat cac ccc atc ttc cga gaa ggt gcc aag Ser Ser Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly Ala Lys 855 860 865	2649
gcc acc ttc atg atc aca ttt gat gtc tcc tac aag gcc ttc ctg gga Ala Thr Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe Leu Gly 870 875 880	2697
gac agg ttg ctt ctg agg gcc agc gca agc agt gag aat aat aag cct Asp Arg Leu Leu Leu Arg Ala Ser Ala Ser Ser Glu Asn Asn Lys Pro 885 890 895	2745
gaa acc agc aag act gcc ttc cag ctg gag ctt ccg gtg aag tac acg Glu Thr Ser Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys Tyr Thr 900 905 910	2793
gtc tat acc gtg atc agt agg cag gaa gat tct acc aag cat ttc aac Val Tyr Thr Val Ile Ser Arg Gln Glu Asp Ser Thr Lys His Phe Asn 915 920 925 930	2841
ttc tca tct tcc cac ggg gag aga cag aaa gag gcc gaa cat cga tat	2889

Phe Ser Ser Ser His Gly Glu Arg Gln Lys Glu Ala Glu His Arg Tyr
935 940 945

cgt gtg aat aac ctg agt cca ttg acg ctg gcc atc agc gtt aac ttc 2937
Arg Val Asn Asn Leu Ser Pro Leu Thr Leu Ala Ile Ser Val Asn Phe
950 955 960

tgg gtc ccc atc ctt ctg aat ggt gtg gcc gtg tgg gat gtg act ctg 2985
Trp Val Pro Ile Leu Leu Asn Gly Val Ala Val Trp Asp Val Thr Leu
965 970 975

agg agc cca gca cag ggt gtc tcc tgt gtg tca cag agg gaa cct cct 3033
Arg Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Arg Glu Pro Pro
980 985 990

caa cat tcc gac ctt ctg acc cag atc caa gga cgc tct gtg ctg gac 3081
Gln His Ser Asp Leu Leu Thr Gln Ile Gln Gly Arg Ser Val Leu Asp
995 1000 1005 1010

tgc gcc atc gcc gac tgc ctg cac ctc cgc tgt gac atc ccc tcc ttg 3129
Cys Ala Ile Ala Asp Cys Leu His Leu Arg Cys Asp Ile Pro Ser Leu
1015 1020 1025

ggc acc ctg gat gag ctt gac ttc att ctg aag ggc aac ctc agc ttc 3177
Gly Thr Leu Asp Glu Leu Asp Phe Ile Leu Lys Gly Asn Leu Ser Phe
1030 1035 1040

ggc tgg atc agt cag aca ttg cag aaa aag gtg ttg ctc ctg agt gag 3225
Gly Trp Ile Ser Gln Thr Leu Gln Lys Val Leu Leu Ser Glu
1045 1050 1055

gct gaa atc aca ttc aac aca tct gtg tat tcc cag ctg ccg gga cag 3273
Ala Glu Ile Thr Phe Asn Thr Ser Val Tyr Ser Gln Leu Pro Gly Gln
1060 1065 1070

gag gca ttt ctg aga gcc cag gtg tca acg atg cta gaa gaa tac gtg 3321
Glu Ala Phe Leu Arg Ala Gln Val Ser Thr Met Leu Glu Glu Tyr Val
1075 1080 1085 1090

gtc tat gag ccc gtc ttc ctc atg gtg ttc agc tca gtg gga ggt ctg 3369
Val Tyr Glu Pro Val Phe Leu Met Val Phe Ser Ser Val Gly Gly Leu
1095 1100 1105

ctg tta ctg gct ctc atc act gtg gcg ctg tac aag ctt ggc ttc ttc 3417
Leu Leu Leu Ala Leu Ile Thr Val Ala Leu Tyr Lys Leu Gly Phe Phe
1110 1115 1120

aaa cgt cag tat aaa gag atg ctg gat cta cca tct gca gat cct gac 3465
Lys Arg Gln Tyr Lys Glu Met Leu Asp Leu Pro Ser Ala Asp Pro Asp
1125 1130 1135

cca gcc ggc cag gca gat tcc aac cat gag act cct cca cat ctc acg 3513
Pro Ala Gly Gln Ala Asp Ser Asn His Glu Thr Pro Pro His Leu Thr
1140 1145 1150

tcc tag 3519
Ser
1155

<210> 46
<211> 1155

<212> PRT

<213> Mus musculus

<400> 46

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Cys His Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu
20 25 30

Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg
35 40 45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
50 55 60

Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu
65 70 75 80

Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85 90 95

Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala
100 105 110

Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
115 120 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro
130 135 140

Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145 150 155 160

Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys
165 170 175

Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met
180 185 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
195 200 205

Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln
210 215 220

Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu
225 230 235 240

Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile
245 250 255

Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His
260 265 270

Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
275 280 285

Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp
385 390 395 400

Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly
465 470 475 480

Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys
485 490 495

Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
610 615 620

Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625 630 635 640

Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
725 730 735

Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
740 745 750

Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
755 760 765

Cys Glu Gly Asn Leu Gly Val Ser Phe Asn Phe Ser Gly Leu Gln Val
770 775 780

Leu Glu Val Gly Ser Ser Pro Glu Leu Thr Val Thr Val Thr Val Trp
785 790 795 800

Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu Ile Lys Phe Tyr Tyr Pro
805 810 815

Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg Ala Gln Gln Pro His Pro
820 825 830

Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu Pro Thr Gly Gln Glu Ser
835 840 845

Leu Arg Ser Ser Ser Cys Ser Ile Asn His Pro Ile Phe Arg Glu Gly
850 855 860

Ala Lys Ala Thr Phe Met Ile Thr Phe Asp Val Ser Tyr Lys Ala Phe
865 870 875 880

Leu Gly Asp Arg Leu Leu Leu Arg Ala Ser Ala Ser Ser Glu Asn Asn
885 890 895

Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln Leu Glu Leu Pro Val Lys
900 905 910

Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln Glu Asp Ser Thr Lys His
915 920 925

Phe Asn Phe Ser Ser Ser His Gly Glu Arg Gln Lys Glu Ala Glu His
930 935 940

Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu Thr Leu Ala Ile Ser Val
945 950 955 960

Asn Phe Trp Val Pro Ile Leu Leu Asn Gly Val Ala Val Trp Asp Val
965 970 975

Thr Leu Arg Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Arg Glu
980 985 990

Pro Pro Gln His Ser Asp Leu Leu Thr Gln Ile Gln Gly Arg Ser Val
995 1000 1005

Leu Asp Cys Ala Ile Ala Asp Cys Leu His Leu Arg Cys Asp Ile Pro
1010 1015 1020

Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe Ile Leu Lys Gly Asn Leu
025 1030 1035 1040

Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln Lys Lys Val Leu Leu Leu
1045 1050 1055

Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser Val Tyr Ser Gln Leu Pro
1060 1065 1070

Gly Gln Glu Ala Phe Leu Arg Ala Gln Val Ser Thr Met Leu Glu Glu
1075 1080 1085

Tyr Val Val Tyr Glu Pro Val Phe Leu Met Val Phe Ser Ser Val Gly
1090 1095 1100

Gly Leu Leu Leu Leu Ala Leu Ile Thr Val Ala Leu Tyr Lys Leu Gly
105 1110 1115 1120

Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu Asp Leu Pro Ser Ala Asp
1125 1130 1135

Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn His Glu Thr Pro Pro His
1140 1145 1150

Leu Thr Ser
115

<210> 47
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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agttaacggat ccggcaccat gaccttcggc actgtgatcc tcctgtgtg

49

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48
gctggacgat ggcatccac 19

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
gttagagttac ggatccggca ccat 24

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
gcagccagct tcggacagac 20

<210> 51
<211> 21
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<220>
<223> Description of Artificial Sequence: primer

<400> 51
ccatgtccac agaacagaga g 21

<210> 52
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<220>
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<222> (1)..(3483)

<220>
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Met Val Arg Gly Val Val Ile Leu Leu Cys Gly Trp Ala Leu Ala Ser
1 5 10 15

tgt cat ggg tct aac ctg gat gtg gag aag ccc gtc gtg ttc aaa gag 96
Cys His Gly Ser Asn Leu Asp Val Glu Lys Pro Val Val Phe Lys Glu
20 25 30

gat gca gcc agc ttc gga cag act gtg gtg cag ttt ggt gga tct cga	Asp Ala Ala Ser Phe Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg	144	
35	40	45	
ctc gtg gga gcc cct ctg gag gcg gtg gca gtc aac caa aca gga	Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly	192	
50	55	60	
cag tcg tct gac tgt ccg cct gcc act ggc gtg tgc cag ccc atc tta	Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu	240	
65	70	75	80
ctg cac att ccc cta gag gca gtg aac atg tcc ctg ggc ctg tct ctg	Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu	288	
85	90	95	
gtg gct gac acc aat aac tcc cag ttg ctg gct tgt ggt cca act gca	Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala	336	
100	105	110	
cag aga gct tgt gca aag aac atg tat gca aaa ggt tcc tgc ctc ctt	Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu	384	
115	120	125	
ctg ggc tcc agc ttg cag ttc atc cag gca atc cct gct acc atg cca	Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro	432	
130	135	140	
gag tgt cca gga caa gag atg gac att gct ttc ctg att gat ggc tcc	Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser	480	
145	150	155	160
ggc agc att gat caa agt gac ttt acc cag atg aag gac ttc gtc aaa	Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys	528	
165	170	175	
gct ttg atg ggc cag ttg gcg agc acc agc acc tcg ttc tcc ctg atg	Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met	576	
180	185	190	
caa tac tca aac atc ctg aag act cat ttt acc ttc acg gaa ttc aag	Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys	624	
195	200	205	
agc agc ctg agc cct cag agc ctg gtg gat gcc atc gtc cag ctc caa	Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln	672	
210	215	220	
ggc ctg acg tac aca gcc tcg ggc atc cag aaa gtg gtg aaa gag cta	Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu	720	
225	230	235	240
ttt cat agc aag aat ggg gcc cga aaa agt gcc aag aag ata cta att	Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile	768	
245	250	255	
gtc atc aca gat ggg cag aaa ttc aga gac ccc ctg gag tat aga cat	Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His	816	
260	265	270	

gtc atc cct gaa gca gag aaa gct ggg atc att cgc tat gct ata ggg Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly 275 280 285	864
gtg gga gat gcc ttc cgg gaa ccc act gcc cta cag gag ctg aac acc Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr 290 295 300	912
att ggc tca gct ccc tcg cag gac cac gtg ttc aag gtg ggc aat ttt Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe 305 310 315 320	960
gta gca ctt cgc agc atc cag cgg caa att cag gag aaa atc ttt gcc Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala 325 330 335	1008
att gaa gga acc gaa tca agg tca agt agt tcc ttt cag cac gag atg Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Phe Gln His Glu Met 340 345 350	1056
tca caa gaa ggt ttc agc tca gct ctc tca atg gat gga cca gtt ctg Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu 355 360 365	1104
ggg gct gtg gga ggc ttc agc tgg tct gga ggt gcc ttc ttg tac ccc Gly Ala Val Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro 370 375 380	1152
tca aat atg aga tcc acc ttc atc aac atg tct cag gag aac gag gat Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp 385 390 395 400	1200
atg agg gac gct tac ctg ggt tac tcc acc gca ctg gcc ttt tgg aag Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys 405 410 415	1248
ggg gtc cac agc ctg atc ctg ggg gcc cct cgc cac cag cac acg ggg Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly 420 425 430	1296
aag gtt gtc atc ttt acc cag gaa tcc agg cac tgg agg ccc aag tct Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser 435 440 445	1344
gaa gtc aga ggg aca cag atc ggc tcc tac ttt ggg gca tct ctc tgt Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys 450 455 460	1392
tct gtg gac atg gat aga gat ggc agc act gac ctg gtc ctg att gga Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly 465 470 475 480	1440
gtc ccc cat tac tat gag cac acc cga ggg ggg cag gtg tcg gtg tgc Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys 485 490 495	1488
ccc atg cct ggt gtg agg agc agg tgg cat tgt ggg acc acc ctc cat Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His 500 505 510	1536

ggg gag cag ggc cat cct tgg ggc cgc ttt ggg gcg gct ctg aca gta 1584
Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
515 520 525

cta ggg gac gtg aat ggg gac agt ctg gcg gat gtg gct att ggt gca 1632
Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

ccc gga gag gag aac aca ggt gct gtc tac ata ttt cat gga gcc 1680
Pro Gly Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

tcg aga cag gac atc gct ccc tcg cct agc cag cgg gtc act ggc tcc 1728
Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

cag ctc ttc ctg agg ctc caa tat ttt ggg cag tca tta agt ggg ggt 1776
Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

cag gac ctt aca cag gat ggc ctg gtg gac ctg gcc gtg gga gcc cag 1824
Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

ggg cac gtg ctg ctg ctt agg agt ctg cct ttg ctg aaa gtg ggg atc 1872
Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
610 615 620

tcc att aga ttt gcc ccc tca gag gtg gca aag act gtg tac cag tgc 1920
Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625 630 635 640

tgg gga agg act ccc act gtc ctc gaa gct gga gag gcc acc gtc tgt 1968
Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

ctc act gtc cgc aaa ggt tca cct gac ctg tta ggt gat gtc caa agc 2016
Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
660 665 670

tct gtc agg tat gat ctg gcg ttg gat ccg ggc cgt ctg att tct cgt 2064
Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

gcc att ttt gat gag acg aag aac tgc act ttg acc cga agg aag act 2112
Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Arg Arg Lys Thr
690 695 700

ctg ggg ctt ggt gat cac tgc gaa aca atg aag ctg ctt ttg cca gac 2160
Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705 710 715 720

tgt gtg gag gat gca gtg acc cct atc atc ctg cgc ctt aac tta tcc 2208
Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
725 730 735

ctg gca ggg gac tct gct cca tcc agg aac ctt cgt cct gtg ctg gct 2256
Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
740 745 750

gtg ggc tca caa gac cat gta aca gct tct ttc ccg ttt gag aag aac 2304
Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
755 760 765

tgt aag cag gag ctc ctg tgt gag ggg aac ctg ggc gtc agc ttc aac 2352
Cys Lys Gln Glu Leu Leu Cys Glu Gly Asn Leu Gly Val Ser Phe Asn
770 775 780

ttc tca ggc ctg cag gtc ttg gag gta gga agc tcc cca gag ctc act 2400
Phe Ser Gly Leu Gln Val Leu Glu Val Gly Ser Ser Pro Glu Leu Thr
785 790 795 800

gtg aca gta aca gtt tgg aat gag ggt gag gac agc tat gga acc tta 2448
Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
805 810 815

atc aag ttc tac tac cca gca gag cta tct tac cga cgg gtg aca aga 2496
Ile Lys Phe Tyr Tyr Pro Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg
820 825 830

gcc cag caa cct cat ccg tac cca cta cgc ctg gca tgt gag gct gag 2544
Ala Gln Gln Pro His Pro Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
835 840 845

ccc acg ggc cag gag agc ctg agg agc agc agc tgt agc atc aat cac 2592
Pro Thr Gly Gln Glu Ser Leu Arg Ser Ser Cys Ser Ile Asn His
850 855 860

ccc atc ttc cga gaa ggt gcc aag gcc acc ttc atg atc aca ttt gat 2640
Pro Ile Phe Arg Glu Gly Ala Lys Ala Thr Phe Met Ile Thr Phe Asp
865 870 875 880

gtc tcc tac aag gcc ttc ctg gga gac agg ttg ctt ctg agg gcc agc 2688
Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Arg Ala Ser
885 890 895

gca agc agt gag aat aat aag cct gaa acc agc aag act gcc ttc cag 2736
Ala Ser Ser Glu Asn Asn Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln
900 905 910

ctg gag ctt ccg gtg aag tac acg gtc tat acc gtg atc agt agg cag 2784
Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln
915 920 925

gaa gat tct acc aag cat ttc aac ttc tca tct tcc cac ggg gag aga 2832
Glu Asp Ser Thr Lys His Phe Asn Phe Ser Ser His Gly Glu Arg
930 935 940

cag aaa gag gcc gaa cat cga tat cgt gtg aat aac ctg agt cca ttg 2880
Gln Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945 950 955 960

acg ctg gcc atc agc gtt aac ttc tgg gtc ccc atc ctt ctg aat ggt 2928
Thr Leu Ala Ile Ser Val Asn Phe Trp Val Pro Ile Leu Leu Asn Gly
965 970 975

gtg gcc gtg tgg gat gtg act ctg agg agc cca gca cag ggt gtc tcc 2976
Val Ala Val Trp Asp Val Thr Leu Arg Ser Pro Ala Gln Gly Val Ser
980 985 990

tgt gtg tca cag agg gaa cct cct caa cat tcc gac ctt ctg acc cag 3024
Cys Val Ser Gln Arg Glu Pro Pro Gln His Ser Asp Leu Leu Thr Gln
995 1000 1005

atc caa gga cgc tct gtg ctg gac tgc gcc atc gcc gac tgc ctg cac 3072
Ile Gln Gly Arg Ser Val Leu Asp Cys Ala Ile Ala Asp Cys Leu His
1010 1015 1020

ctc cgc tgt gac atc ccc tcc ttg ggc acc ctg gat gag ctt gac ttc 3120
Leu Arg Cys Asp Ile Pro Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe
1025 1030 1035 1040

att ctg aag ggc aac ctc agc ttc ggc tgg atc agt cag aca ttg cag 3168
Ile Leu Lys Gly Asn Leu Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln
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aaa aag gtg ttg ctc ctg agt gag gct gaa atc aca ttc aac aca tct 3216
Lys Lys Val Leu Leu Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser
1060 1065 1070

gtg tat tcc cag ctg ccg gga cag gag gca ttt ctg aga gcc cag gtg 3264
Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
1075 1080 1085

tca acg atg cta gaa gaa tac gtg gtc tat gag ccc gtc ttc ctc atg 3312
Ser Thr Met Leu Glu Glu Tyr Val Val Tyr Glu Pro Val Phe Leu Met
1090 1095 1100

gtg ttc agc tca gtg gga ggt ctg ctg tta ctg gct ctc atc act gtg 3360
Val Phe Ser Ser Val Gly Gly Leu Leu Leu Ala Leu Ile Thr Val
1105 1110 1115 1120

gcg ctg tac aag ctt ggc ttc aaa cgt cag tat aaa gag atg ctg 3408
Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu
1125 1130 1135

gat cta cca tct gca gat cct gac cca gcc ggc cag gca gat tcc aac 3456
Asp Leu Pro Ser Ala Asp Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn
1140 1145 1150

cat gag act cct cca cat ctc acg tcc taggaatcta ctttcctgtta 3503
His Glu Thr Pro Pro His Leu Thr Ser
1155 1160

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35 40 45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
50 55 60

Gln Ser Ser Asp Cys Pro Pro Ala Thr Gly Val Cys Gln Pro Ile Leu
65 70 75 80

Leu His Ile Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85 90 95

Val Ala Asp Thr Asn Asn Ser Gln Leu Leu Ala Cys Gly Pro Thr Ala
100 105 110

Gln Arg Ala Cys Ala Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
115 120 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Ile Pro Ala Thr Met Pro
130 135 140

Glu Cys Pro Gly Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145 150 155 160

Gly Ser Ile Asp Gln Ser Asp Phe Thr Gln Met Lys Asp Phe Val Lys
165 170 175

Ala Leu Met Gly Gln Leu Ala Ser Thr Ser Thr Ser Phe Ser Leu Met
180 185 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
195 200 205

Ser Ser Leu Ser Pro Gln Ser Leu Val Asp Ala Ile Val Gln Leu Gln
210 215 220

Gly Leu Thr Tyr Thr Ala Ser Gly Ile Gln Lys Val Val Lys Glu Leu
225 230 235 240

Phe His Ser Lys Asn Gly Ala Arg Lys Ser Ala Lys Lys Ile Leu Ile
245 250 255

Val Ile Thr Asp Gly Gln Lys Phe Arg Asp Pro Leu Glu Tyr Arg His
260 265 270

Val Ile Pro Glu Ala Glu Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
275 280 285

Val Gly Asp Ala Phe Arg Glu Pro Thr Ala Leu Gln Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Ser Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Val Ala Leu Arg Ser Ile Gln Arg Gln Ile Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Glu Ser Arg Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Ser Met Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Gly Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Ser Asn Met Arg Ser Thr Phe Ile Asn Met Ser Gln Glu Asn Glu Asp
385 390 395 400

Met Arg Asp Ala Tyr Leu Gly Tyr Ser Thr Ala Leu Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ser Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Met Asp Arg Asp Gly Ser Thr Asp Leu Val Leu Ile Gly
465 470 475 480

Val Pro His Tyr Tyr Glu His Thr Arg Gly Gly Gln Val Ser Val Cys
485 490 495

Pro Met Pro Gly Val Arg Ser Arg Trp His Cys Gly Thr Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Ala Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Ser Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Asn Arg Gly Ala Val Tyr Ile Phe His Gly Ala
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Ser Arg Gln Asp Ile Ala Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Phe Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Gly Ile
610 615 620

Ser Ile Arg Phe Ala Pro Ser Glu Val Ala Lys Thr Val Tyr Gln Cys
625 630 635 640

Trp Gly Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val Arg Lys Gly Ser Pro Asp Leu Leu Gly Asp Val Gln Ser
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Arg Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Met Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Thr Pro Ile Ile Leu Arg Leu Asn Leu Ser
725 730 735

Leu Ala Gly Asp Ser Ala Pro Ser Arg Asn Leu Arg Pro Val Leu Ala
740 745 750

Val Gly Ser Gln Asp His Val Thr Ala Ser Phe Pro Phe Glu Lys Asn
755 760 765

Cys Lys Gln Glu Leu Leu Cys Glu Gly Asn Leu Gly Val Ser Phe Asn
770 775 780

Phe Ser Gly Leu Gln Val Leu Glu Val Gly Ser Ser Pro Glu Leu Thr
785 790 795 800

Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
805 810 815

Ile Lys Phe Tyr Tyr Pro Ala Glu Leu Ser Tyr Arg Arg Val Thr Arg
820 825 830

Ala Gln Gln Pro His Pro Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
835 840 845

Pro Thr Gly Gln Glu Ser Leu Arg Ser Ser Ser Cys Ser Ile Asn His
850 855 860

Pro Ile Phe Arg Glu Gly Ala Lys Ala Thr Phe Met Ile Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Ser
885 890 895

Ala Ser Ser Glu Asn Asn Lys Pro Glu Thr Ser Lys Thr Ala Phe Gln
900 905 910

Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Val Ile Ser Arg Gln
915 920 925

Glu Asp Ser Thr Lys His Phe Asn Phe Ser Ser Ser His Gly Glu Arg
930 935 940

Gln Lys Glu Ala Glu His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945 950 955 960

Thr Leu Ala Ile Ser Val Asn Phe Trp Val Pro Ile Leu Leu Asn Gly
965 970 975

Val Ala Val Trp Asp Val Thr Leu Arg Ser Pro Ala Gln Gly Val Ser
980 985 990

Cys Val Ser Gln Arg Glu Pro Pro Gln His Ser Asp Leu Leu Thr Gln
995 1000 1005

Ile Gln Gly Arg Ser Val Leu Asp Cys Ala Ile Ala Asp Cys Leu His
1010 1015 1020

Leu Arg Cys Asp Ile Pro Ser Leu Gly Thr Leu Asp Glu Leu Asp Phe
1025 1030 1035 1040

Ile Leu Lys Gly Asn Leu Ser Phe Gly Trp Ile Ser Gln Thr Leu Gln
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Lys Lys Val Leu Leu Ser Glu Ala Glu Ile Thr Phe Asn Thr Ser
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Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
1075 1080 1085

Ser Thr Met Leu Glu Glu Tyr Val Val Tyr Glu Pro Val Phe Leu Met
1090 1095 1100

Val Phe Ser Ser Val Gly Gly Leu Leu Leu Ala Leu Ile Thr Val
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Ala Leu Tyr Lys Leu Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Leu
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Asp Leu Pro Ser Ala Asp Pro Asp Pro Ala Gly Gln Ala Asp Ser Asn
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His Glu Thr Pro Pro His Leu Thr Ser
1155 1160

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<211> 3597
<212> DNA
<213> Rattus rattus

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Val Ile Leu Leu Cys Gly Trp Val Leu Ala Ser Cys His Gly Ser Asn
10 15 20

ctg gat gtg gag gaa ccc atc gtg ttc aga gag gat gca gcc agc ttt 150
Leu Asp Val Glu Glu Pro Ile Val Phe Arg Glu Asp Ala Ala Ser Phe
25 30 35

gga cag act gtg gtg cag ttt ggt gga tct cga ctc gtg gtg gga gcc 198
Gly Gln Thr Val Val Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala
40 45 50

cct ctg gag gcg gtg gca gtc aac caa aca gga cgg ttg tat gac tgt 246
Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly Arg Leu Tyr Asp Cys
55 60 65

gca cct gcc act ggc atg tgc cag ccc atc gta ctg cgc agt ccc cta 294
Ala Pro Ala Thr Gly Met Cys Gln Pro Ile Val Leu Arg Ser Pro Leu
70 75 80 85

gag gca gtg aac atg tcc ctg ggc ctg tct ctg gtg act gcc acc aat 342
Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Val Thr Ala Thr Asn
90 95 100

aac gcc cag ttg ctg gct tgt ggt cca act gca cag aga gct tgt gtg 390
Asn Ala Gln Leu Leu Ala Cys Gly Pro Thr Ala Gln Arg Ala Cys Val
105 110 115

aag aac atg tat gcg aaa ggt tcc tgc ctc ctt ctc ggc tcc agc ttg 438
Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu Leu Gly Ser Ser Leu
120 125 130

cag ttc atc cag gca gtc cct gcc tcc atg cca gag tgt cca aga caa 486
Gln Phe Ile Gln Ala Val Pro Ala Ser Met Pro Glu Cys Pro Arg Gln
135 140 145

gag atg gac att gct ttc ctg att gat ggt tct ggc agc att aac caa 534
Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser Gly Ser Ile Asn Gln
150 155 160 165

agg gac ttt gcc cag atg aag gac ttt gtc aaa gct ttg atg gga gag 582
Arg Asp Phe Ala Gln Met Lys Asp Phe Val Lys Ala Leu Met Gly Glu
170 175 180

ttt gcg agc acc agc acc ttg ttc tcc ctg atg caa tac tcg aac atc 630
Phe Ala Ser Thr Ser Thr Leu Phe Ser Leu Met Gln Tyr Ser Asn Ile
185 190 195

ctg aag acc cat ttt acc ttc act gaa ttc aag aac atc ctg gac cct 678
Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys Asn Ile Leu Asp Pro
200 205 210

cag agc ctg gtg gat ccc att gtc cag ctg caa ggc ctg acc tac aca 726
Gln Ser Leu Val Asp Pro Ile Val Gln Leu Gln Gly Leu Thr Tyr Thr
215 220 225

gcc aca ggc atc cgg aca gtg atg gaa gag cta ttt cat agc aag aat 774
Ala Thr Gly Ile Arg Thr Val Met Glu Glu Leu Phe His Ser Lys Asn
230 235 240 245

ggg tcc cgt aaa agt gcc aag aag atc ctc ctt gtc atc aca gat ggg 822
Gly Ser Arg Lys Ser Ala Lys Lys Ile Leu Leu Val Ile Thr Asp Gly
250 255 260

cag aaa tac aga gac ccc ctg gag tat agt gat gtc att ccc gcc gca 870
Gln Lys Tyr Arg Asp Pro Leu Glu Tyr Ser Asp Val Ile Pro Ala Ala
265 270 275

gac aaa gct ggc atc att cgt tat gct att ggg gtg gga gat gcc ttc 918
Asp Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe
280 285 290

cag gag ccc act gcc ctg aag gag ctg aac acc att ggc tca gct ccc 966
Gln Glu Pro Thr Ala Leu Lys Glu Leu Asn Thr Ile Gly Ser Ala Pro
295 300 305

cca cag gac cac gtg ttc aag gta ggc aac ttt gca gca ctt cgc agc 1014
Pro Gln Asp His Val Phe Lys Val Gly Asn Phe Ala Ala Leu Arg Ser
310 315 320 325

atc cag agg caa ctt cag gag aaa atc ttc gcc att gag gga act caa 1062
Ile Gln Arg Gln Leu Gln Glu Lys Ile Phe Ala Ile Glu Gly Thr Gln
330 335 340

tca agg tca agt agt tcc ttt cag cac gag atg tca caa gaa ggt ttc 1110
Ser Arg Ser Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe
345 350 355

agt tca gct ctc aca tcg gat gga ccc gtt ctg ggg gcc gtg gga agc 1158
Ser Ser Ala Leu Thr Ser Asp Gly Pro Val Leu Gly Ala Val Gly Ser
360 365 370

ttc agc tgg tcc gga ggt gcc ttc tta tat ccc cca aat acg aga ccc 1206
Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Asn Thr Arg Pro
375 380 385

acc ttt atc aac atg tct cag gag aat gtg gac atg aga gac tcc tac 1254
Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp Met Arg Asp Ser Tyr
390 395 400 405

ctg ggt tac tcc acc gca gtg gcc ttt tgg aag ggg gtt cac agc ctg 1302
Leu Gly Tyr Ser Thr Ala Val Ala Phe Trp Lys Gly Val His Ser Leu
410 415 420

atc ctg ggg gcc ccg cgt cac cag cac acg ggg aag gtt gtc atc ttt 1350
Ile Leu Gly Ala Pro Arg His Gln His Thr Gly Lys Val Val Ile Phe
425 430 435

acc cag gaa gcc agg cat tgg agg ccc aag tct gaa gtc aga ggg aca 1398
Thr Gln Glu Ala Arg His Trp Arg Pro Lys Ser Glu Val Arg Gly Thr
440 445 450

cag atc ggc tcc tac ttc ggg gcc tct ctc tgt tct gtg gac gtg gat 1446
Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys Ser Val Asp Val Asp
455 460 465

aga gat ggc agc acy gac ctg gtc ctg atc gga gcc ccc cat tac tat 1494
Arg Asp Gly Ser Xaa Asp Leu Val Leu Ile Gly Ala Pro His Tyr Tyr
470 475 480 485

gag cag acc cga ggg ggg cag gtc tca gtg ttc ccc gtg ccc ggt gtg 1542
Glu Gln Thr Arg Gly Gly Gln Val Ser Val Phe Pro Val Pro Gly Val
490 495 500

agg ggc agg tgg cag tgt gag gcc acc ctc cac ggg gag cag ggc cat	1590		
Arg Gly Arg Trp Gln Cys Glu Ala Thr Leu His Gly Glu Gln Gly His			
505	510	515	
cct tgg ggc cgc ttt ggg gtg gct ctg aca gtg ctg ggg gac gta aac	1638		
Pro Trp Gly Arg Phe Gly Val Ala Leu Thr Val Leu Gly Asp Val Asn			
520	525	530	
ggg gac aat ctg gca gac gtg gct att ggt gcc cct gga gag gag gag	1686		
Gly Asp Asn Leu Ala Asp Val Ala Ile Gly Ala Pro Gly Glu Glu			
535	540	545	
agc aga ggt gct gtc tac ata ttt cat gga gcc tcg aga ctg gag atc	1734		
Ser Arg Gly Ala Val Tyr Ile Phe His Gly Ala Ser Arg Leu Glu Ile			
550	555	560	565
atg ccc tca ccc agc cag cgg gtc act ggc tcc cag ctc tcc ctg aga	1782		
Met Pro Ser Pro Ser Gln Arg Val Thr Gly Ser Gln Leu Ser Leu Arg			
570	575	580	
ctg cag tat ttt ggg cag tca ttg agt ggg ggt cag gac ctt aca cag	1830		
Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly Gln Asp Leu Thr Gln			
585	590	595	
gat ggc ctg gtg gac ctg gcc gtg gga gcc cag ggg cac gta ctg ctg	1878		
Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln Gly His Val Leu Leu			
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ctc agg agt ctg cct ctg ctg aaa gtg gag ctc tcc ata aga ttc gcc	1926		
Leu Arg Ser Leu Pro Leu Leu Lys Val Glu Leu Ser Ile Arg Phe Ala			
615	620	625	
ccc atg gag gtg gca aag gct gtg tac cag tgc tgg gaa agg act ccc	1974		
Pro Met Glu Val Ala Lys Ala Val Tyr Gln Cys Trp Glu Arg Thr Pro			
630	635	640	645
act gtc ctc gaa gct gga gag gcc act gtc tgt ctc act gtc cac aaa	2022		
Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys Leu Thr Val His Lys			
650	655	660	
ggc tca cct gac ctg tta ggt aat gtc caa ggc tct gtc agg tat gat	2070		
Gly Ser Pro Asp Leu Leu Gly Asn Val Gln Gly Ser Val Arg Tyr Asp			
665	670	675	
ctg gcg tta gat ccg ggc cgc ctg att tct cgt gcc att ttt gat gag	2118		
Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg Ala Ile Phe Asp Glu			
680	685	690	
act aag aac tgc act ttg acg gga agg aag act ctg ggg ctt ggt gat	2166		
Thr Lys Asn Cys Thr Leu Thr Gly Arg Lys Thr Leu Gly Leu Gly Asp			
695	700	705	
cac tgc gaa aca gtg aag ctg ctt ttg ccg gac tgt gtg gaa gat gca	2214		
His Cys Glu Thr Val Lys Leu Leu Pro Asp Cys Val Glu Asp Ala			
710	715	720	725
gtg agc cct atc atc ctg cgc ctc aac ttt tcc ctg gtg aga gac tct	2262		
Val Ser Pro Ile Ile Leu Arg Leu Asn Phe Ser Leu Val Arg Asp Ser			
730	735	740	

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cac ata act gct tct ctg ccg ttt gag aag aac tgt aag caa gaa ctc His Ile Thr Ala Ser Leu Pro Phe Glu Lys Asn Cys Lys Gln Glu Leu 760 765 770	2358
ctg tgt gag ggg gac ctg ggc atc agc ttt aac ttc tca ggc ctg cag Leu Cys Glu Gly Asp Leu Gly Ile Ser Phe Asn Phe Ser Gly Leu Gln 775 780 785	2406
gtc ttg gtg gtg gga ggc tcc cca gag ctc act gtg aca gtc act gtg Val Leu Val Val Gly Gly Ser Pro Glu Leu Thr Val Thr Val Thr Val 790 795 800 805	2454
tgg aat gag ggt gag gac agc tat gga act tta gtc aag ttc tac tac Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu Val Lys Phe Tyr Tyr 810 815 820	2502
cca gca ggg cta tct tac cga cg ^g gta aca ggg act cag caa cct cat Pro Ala Gly Leu Ser Tyr Arg Arg Val Thr Gly Thr Gln Gln Pro His 825 830 835	2550
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Val Thr Leu Ser Ser Pro Ala Gln Gly Val Ser Cys Val Ser Gln Met
985 990 995

aaa cct cct cag aat ccc gac ttt ctg acc cag att cag aga cgt tct 3078
Lys Pro Pro Gln Asn Pro Asp Phe Leu Thr Gln Ile Gln Arg Arg Ser
1000 1005 1010

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Val Leu Asp Cys Ser Ile Ala Asp Cys Leu His Phe Arg Cys Asp Ile
1015 1020 1025

ccc tcc ttg gac atc cag gat gaa ctt gac ttc att ctg agg ggc aac 3174
Pro Ser Leu Asp Ile Gln Asp Glu Leu Asp Phe Ile Leu Arg Gly Asn
1030 1035 1040 1045

ctc agc ttc ggc tgg gtc agt cag aca ttg cag gaa aag gtg ttg ctt 3222
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1050 1055 1060

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Val Ser Glu Ala Glu Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu
1065 1070 1075

cca gga cag gag gca ttt ctg aga gcc cag gtg gag aca acg tta gaa 3318
Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val Glu Thr Thr Leu Glu
1080 1085 1090

gaa tac gtg gtc tat gag ccc atc ttc ctc gtg gcg ggc agc tcg gtg 3366
Glu Tyr Val Val Tyr Glu Pro Ile Phe Leu Val Ala Gly Ser Ser Val
1095 1100 1105

gga ggt ctg ctg tta ctg gct ctc atc aca gtg gta ctg tac aag ctt 3414
Gly Gly Leu Leu Leu Ala Leu Ile Thr Val Val Leu Tyr Lys Leu
1110 1115 1120 1125

ggc ttc tyc aaa cgt cag tac aaa gaa atg ctg gac ggc aag gct gca 3462
Gly Phe Xaa Lys Arg Gln Tyr Lys Glu Met Leu Asp Gly Lys Ala Ala
1130 1135 1140

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Asp Pro Val Thr Ala Gly Gln Ala Asp Phe Gly Cys Glu Thr Pro Pro
1145 1150 1155

tat ctc gtg agc taggaatcca ctctcctgcc tatctctgca atgaagattg 3562
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gtcctgccta tgagtctact ggcatggaa cgagt 3597

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35 40 45

Leu Val Val Gly Ala Pro Leu Glu Ala Val Ala Val Asn Gln Thr Gly
50 55 60

Arg Leu Tyr Asp Cys Ala Pro Ala Thr Gly Met Cys Gln Pro Ile Val
65 70 75 80

Leu Arg Ser Pro Leu Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85 90 95

Val Thr Ala Thr Asn Asn Ala Gln Leu Leu Ala Cys Gly Pro Thr Ala
100 105 110

Gln Arg Ala Cys Val Lys Asn Met Tyr Ala Lys Gly Ser Cys Leu Leu
115 120 125

Leu Gly Ser Ser Leu Gln Phe Ile Gln Ala Val Pro Ala Ser Met Pro
130 135 140

Glu Cys Pro Arg Gln Glu Met Asp Ile Ala Phe Leu Ile Asp Gly Ser
145 150 155 160

Gly Ser Ile Asn Gln Arg Asp Phe Ala Gln Met Lys Asp Phe Val Lys
165 170 175

Ala Leu Met Gly Glu Phe Ala Ser Thr Ser Thr Leu Phe Ser Leu Met
180 185 190

Gln Tyr Ser Asn Ile Leu Lys Thr His Phe Thr Phe Thr Glu Phe Lys
195 200 205

Asn Ile Leu Asp Pro Gln Ser Leu Val Asp Pro Ile Val Gln Leu Gln
210 215 220

Gly Leu Thr Tyr Thr Ala Thr Gly Ile Arg Thr Val Met Glu Glu Leu
225 230 235 240

Phe His Ser Lys Asn Gly Ser Arg Lys Ser Ala Lys Lys Ile Leu Leu
245 250 255

Val Ile Thr Asp Gly Gln Lys Tyr Arg Asp Pro Leu Glu Tyr Ser Asp
260 265 270

Val Ile Pro Ala Ala Asp Lys Ala Gly Ile Ile Arg Tyr Ala Ile Gly
275 280 285

Val Gly Asp Ala Phe Gln Glu Pro Thr Ala Leu Lys Glu Leu Asn Thr
290 295 300

Ile Gly Ser Ala Pro Pro Gln Asp His Val Phe Lys Val Gly Asn Phe
305 310 315 320

Ala Ala Leu Arg Ser Ile Gln Arg Gln Leu Gln Glu Lys Ile Phe Ala
325 330 335

Ile Glu Gly Thr Gln Ser Arg Ser Ser Ser Phe Gln His Glu Met
340 345 350

Ser Gln Glu Gly Phe Ser Ser Ala Leu Thr Ser Asp Gly Pro Val Leu
355 360 365

Gly Ala Val Gly Ser Phe Ser Trp Ser Gly Gly Ala Phe Leu Tyr Pro
370 375 380

Pro Asn Thr Arg Pro Thr Phe Ile Asn Met Ser Gln Glu Asn Val Asp
385 390 395 400

Met Arg Asp Ser Tyr Leu Gly Tyr Ser Thr Ala Val Ala Phe Trp Lys
405 410 415

Gly Val His Ser Leu Ile Leu Gly Ala Pro Arg His Gln His Thr Gly
420 425 430

Lys Val Val Ile Phe Thr Gln Glu Ala Arg His Trp Arg Pro Lys Ser
435 440 445

Glu Val Arg Gly Thr Gln Ile Gly Ser Tyr Phe Gly Ala Ser Leu Cys
450 455 460

Ser Val Asp Val Asp Arg Asp Gly Ser Xaa Asp Leu Val Leu Ile Gly
465 470 475 480

Ala Pro His Tyr Tyr Glu Gln Thr Arg Gly Gly Gln Val Ser Val Phe
485 490 495

Pro Val Pro Gly Val Arg Gly Arg Trp Gln Cys Glu Ala Thr Leu His
500 505 510

Gly Glu Gln Gly His Pro Trp Gly Arg Phe Gly Val Ala Leu Thr Val
515 520 525

Leu Gly Asp Val Asn Gly Asp Asn Leu Ala Asp Val Ala Ile Gly Ala
530 535 540

Pro Gly Glu Glu Glu Ser Arg Gly Ala Val Tyr Ile Phe His Gly Ala
545 550 555 560

Ser Arg Leu Glu Ile Met Pro Ser Pro Ser Gln Arg Val Thr Gly Ser
565 570 575

Gln Leu Ser Leu Arg Leu Gln Tyr Phe Gly Gln Ser Leu Ser Gly Gly
580 585 590

Gln Asp Leu Thr Gln Asp Gly Leu Val Asp Leu Ala Val Gly Ala Gln
595 600 605

Gly His Val Leu Leu Leu Arg Ser Leu Pro Leu Leu Lys Val Glu Leu
610 615 620

Ser Ile Arg Phe Ala Pro Met Glu Val Ala Lys Ala Val Tyr Gln Cys
625 630 635 640

Trp Glu Arg Thr Pro Thr Val Leu Glu Ala Gly Glu Ala Thr Val Cys
645 650 655

Leu Thr Val His Lys Gly Ser Pro Asp Leu Leu Gly Asn Val Gln Gly
660 665 670

Ser Val Arg Tyr Asp Leu Ala Leu Asp Pro Gly Arg Leu Ile Ser Arg
675 680 685

Ala Ile Phe Asp Glu Thr Lys Asn Cys Thr Leu Thr Gly Arg Lys Thr
690 695 700

Leu Gly Leu Gly Asp His Cys Glu Thr Val Lys Leu Leu Leu Pro Asp
705 710 715 720

Cys Val Glu Asp Ala Val Ser Pro Ile Ile Leu Arg Leu Asn Phe Ser
725 730 735

Leu Val Arg Asp Ser Ala Ser Pro Arg Asn Leu His Pro Val Leu Ala
740 745 750

Val Gly Ser Gln Asp His Ile Thr Ala Ser Leu Pro Phe Glu Lys Asn
755 760 765

Cys Lys Gln Glu Leu Leu Cys Glu Gly Asp Leu Gly Ile Ser Phe Asn
770 775 780

Phe Ser Gly Leu Gln Val Leu Val Val Gly Gly Ser Pro Glu Leu Thr
785 790 795 800

Val Thr Val Thr Val Trp Asn Glu Gly Glu Asp Ser Tyr Gly Thr Leu
805 810 815

Val Lys Phe Tyr Tyr Pro Ala Gly Leu Ser Tyr Arg Arg Val Thr Gly
820 825 830

Thr Gln Gln Pro His Gln Tyr Pro Leu Arg Leu Ala Cys Glu Ala Glu
835 840 845

Pro Ala Ala Gln Glu Asp Leu Arg Ser Ser Ser Cys Ser Ile Asn His
850 855 860

Pro Ile Phe Arg Glu Gly Ala Lys Thr Thr Phe Met Ile Thr Phe Asp
865 870 875 880

Val Ser Tyr Lys Ala Phe Leu Gly Asp Arg Leu Leu Leu Arg Ala Lys
885 890 895

Ala Ser Ser Glu Asn Asn Lys Pro Asp Thr Asn Lys Thr Ala Phe Gln
900 905 910

Leu Glu Leu Pro Val Lys Tyr Thr Val Tyr Thr Leu Ile Ser Arg Gln
915 920 925

Glu Asp Ser Thr Asn His Val Asn Phe Ser Ser Ser His Gly Gly Arg
930 935 940

Arg Gln Glu Ala Ala His Arg Tyr Arg Val Asn Asn Leu Ser Pro Leu
945 950 955 960

Lys Leu Ala Val Arg Val Asn Phe Trp Val Pro Val Leu Leu Asn Gly
965 970 975

Val Ala Val Trp Asp Val Thr Leu Ser Ser Pro Ala Gln Gly Val Ser
980 985 990

Cys Val Ser Gln Met Lys Pro Pro Gln Asn Pro Asp Phe Leu Thr Gln
995 1000 1005

Ile Gln Arg Arg Ser Val Leu Asp Cys Ser Ile Ala Asp Cys Leu His
1010 1015 1020

Phe Arg Cys Asp Ile Pro Ser Leu Asp Ile Gln Asp Glu Leu Asp Phe
025 1030 1035 1040

Ile Leu Arg Gly Asn Leu Ser Phe Gly Trp Val Ser Gln Thr Leu Gln
1045 1050 1055

Glu Lys Val Leu Leu Val Ser Glu Ala Glu Ile Thr Phe Asp Thr Ser
1060 1065 1070

Val Tyr Ser Gln Leu Pro Gly Gln Glu Ala Phe Leu Arg Ala Gln Val
1075 1080 1085

Glu Thr Thr Leu Glu Glu Tyr Val Val Tyr Glu Pro Ile Phe Leu Val
1090 1095 1100

Ala Gly Ser Ser Val Gly Gly Leu Leu Leu Ala Leu Ile Thr Val
105 1110 1115 1120

Val Leu Tyr Lys Leu Gly Phe Xaa Lys Arg Gln Tyr Lys Glu Met Leu
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Asp Gly Lys Ala Ala Asp Pro Val Thr Ala Gly Gln Ala Asp Phe Gly
1140 1145 1150

Cys Glu Thr Pro Pro Tyr Leu Val Ser
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<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 56

cctgtcatgg gtctaacctg

20

<210> 57

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 57

aggtagacc catgacagg

19

<210> 58
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
ggccttgcag ctggacaatg 20

<210> 59
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
ccaaagctgg ctgcatcctc tc 22

<210> 60
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 60
ccgcctgcca ctggcgttg c 21

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 61
cccagatgaa ggacttcgtc aa 22

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 62
gctgggatca ttcgctatgc 20

<210> 63
<211> 21

<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 63
caatggatgg accagttctg g 21

<210> 64
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<220>
<223> Description of Artificial Sequence: primer

<400> 64
cagatcggtt cctactttgg 20

<210> 65
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 65
catggagcct cgagacagg 19

<210> 66
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 66
ccactgtcct cgaagctgga g 21

<210> 67
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 67
cttcgtcctg tgctggctgt gggctc 26

<210> 68
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

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cgccctggcat gtgaggctga g 21

<210> 69
<211> 21
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<220>
<223> Description of Artificial Sequence: primer

<400> 69
ccgtgatcag taggcaggaa g 21

<210> 70
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 70
gtcacagagg gaacctcc 18

<210> 71
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 71
gctcctgagt gaggttgaaa tca 23

<210> 72
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 72
gagatgctgg atctaccatc tgc 23

<210> 73
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 73
ctgagctggg agattttat gg 22

<210> 74
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 74
gtggatcagc actgaaatct g 21

<210> 75
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 75
cgtttgaaga agccaaagttt g 21

<210> 76
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 76
cacagcggag gtgcaggcag 20

<210> 77
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 77
ctcaactgctt gcgcgtggc 18

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 78
cggttaagata gctctgtgg 20

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 79
gagcccacag ccagcacagg 20

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 80
gatccaaacgc cagatcatac c 21

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 81
cacggccagg tccaccaggc 20

<210> 82
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 82
cacgtccccct agcactgtca g 21

<210> 83
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 83
ttgacgaagt ccttcatctg gg 22

<210> 84

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 84
gaactgcaag ctggagccca g

21

<210> 85
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 85
ctggatgctg cgaagtgcta c

21

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 86
gccttggagc tggacgtgg c

21

<210> 87
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 87
gtaagatctc cagagtgtcc aagacaagag atg

33

<210> 88
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
cttctcgagt gtgagagctg aactgaaacc ttc

33

<210> 89
<211> 32
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 89

cgctgtacg tcagagttga gtccaaatat gg

32

<210> 90

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 90

ggtgacacta tagaataggg c

21

<210> 91

<211> 18

<212> DNA

<213> Mus musculus

<400> 91

aaggcaggagc tcctgtgt

18

<210> 92

<211> 852

<212> DNA

<213> rabbit

<220>

<221> CDS

<222> (61)..(852)

<400> 92

tgcatccctt ccaggccact gttccctctc cacttcccctt caccgctgca ctgctcagag 60

atg gcc ctt ggg gct gtg gtc ctc ctt ggg gtc ctg gct tct tac cac 108
Met Ala Leu Gly Ala Val Val Leu Leu Gly Val Leu Ala Ser Tyr His
1 5 10 15

gga ttc aac ttg gac gtg atg agc ggt gat ctt cca gga aga cgc agc 156
Gly Phe Asn Leu Asp Val Met Ser Gly Asp Leu Pro Gly Arg Arg Ser
20 25 30

ggg ctt cgg gca gag cgt gat gca gtt tgg gga tct cga ctc gtg gtg 204
Gly Leu Arg Ala Glu Arg Asp Ala Val Trp Gly Ser Arg Leu Val Val
35 40 45

gga gcc ccc ctg gcg gtg gtg tcg gcc aac cac aca gga cgg ctg tac 252
Gly Ala Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg Leu Tyr
50 55 60

gag tgt gcg cct gcc tcc ggc acc tgc acg ccc att ttc cca ttc atg 300
Glu Cys Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro Phe Met
65 70 75 80

ccc ccc gaa gcc gtg aac atg tcc ctg ggc ctg tcc ctg gca gcc tcc Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Ser 85 90 95	348
ccc aac cat tcc cag ctg ctg gct tgt ggc ccg acc gtg cat aga gcc Pro Asn His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His Arg Ala 100 105 110	396
tgc ggg gag gac gtg tac gcc cag ggt ttc tgt gtg ctg ctg gat gcc Cys Gly Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu Asp Ala 115 120 125	444
cac gca cag ccc atc ggg act gtg cca gct gcc ctg ccc gag tgc cca His Ala Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu Cys Pro 130 135 140	492
gat caa gag atg gac att gtc ttc ctg att gac ggc tct ggc agc att Asp Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile 145 150 155 160	540
agc tca aat gac ttc cgc aag atg aag gac ttt gtc aga gct gtg atg Ser Ser Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala Val Met 165 170 175	588
gac cag ttc aag gac acc aac acc cag ttc tcg ctg atg cag tac tcc Asp Gln Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln Tyr Ser 180 185 190	636
aat gtg ctg gtg aca cat ttc acc ttc agc agc ttc cgg aac agc tcc Asn Val Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn Ser Ser 195 200 205	684
aat cct cag ggc cta gtg gag ccc att gtg cag ctg aca ggc ctc acg Asn Pro Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly Leu Thr 210 215 220	732
ttc acg gcc aca ggg atc ctg aaa gtg gtg aca gag ctg ttt caa acc Phe Thr Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe Gln Thr 225 230 235 240	780
aag aac ggg gcc cgc gaa agt gcc aag aag atc ctc atc gtc atc aca Lys Asn Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val Ile Thr 245 250 255	828
gat ggg cag aag tac aaa gcg gca Asp Gly Gln Lys Tyr Lys Ala Ala 260	852
<210> 93 <211> 264 <212> PRT <213> rabbit	
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Gly Leu Arg Ala Glu Arg Asp Ala Val Trp Gly Ser Arg Leu Val Val
35 40 45

Gly Ala Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg Leu Tyr
50 55 60

Glu Cys Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro Phe Met
65 70 75 80

Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Ser
85 90 95

Pro Asn His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His Arg Ala
100 105 110

Cys Gly Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu Asp Ala
115 120 125

His Ala Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu Cys Pro
130 135 140

Asp Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile
145 150 155 160

Ser Ser Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala Val Met
165 170 175

Asp Gln Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln Tyr Ser
180 185 190

Asn Val Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn Ser Ser
195 200 205

Asn Pro Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly Leu Thr
210 215 220

Phe Thr Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe Gln Thr
225 230 235 240

Lys Asn Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val Ile Thr
245 250 255

Asp Gly Gln Lys Tyr Lys Ala Ala
260

<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
ctgggtctgga ggtgccttcc tg

22

<210> 95
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 95

cctgagcagg agcacctggc c

21

<210> 96

<211> 2499

<212> DNA

<213> Homo sapiens

<400> 96

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cagttcggtg gatctcgact cgtggtgaa gcaccccctgg aggtggtgcc ggccaaccag 180
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<212> DNA
<213> Homo sapiens

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Gly Ala Val Val Leu Leu Gly Val Leu Ala Ser Tyr
1 5 10

cac gga ttc aac ttg gac gtg gat gag ccg gtg atc ttc cag gaa gac	100
His Gly Phe Asn Leu Asp Val Asp Glu Pro Val Ile Phe Gln Glu Asp	
15 20 25	
gca gcg ggc ttc ggg cag agc gtg atg cag ttt gga gga tct cga ctc	148
Ala Ala Gly Phe Gly Gln Ser Val Met Gln Phe Gly Gly Ser Arg Leu	
30 35 40	
gtg gtg gga gcc ccc ctg gcg gtg tcg gcc aac cac aca gga cgg	196
Val Val Gly Ala Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg	
45 50 55 60	
ctg tac gag tgt gcg cct gcc tcc ggc acc tgc acg ccc att ttc cca	244
Leu Tyr Glu Cys Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro	
65 70 75	
ttc atg ccc ccc gaa gcc gtg aac atg tcc ctg ggc ctg tcc ctg gca	292
Phe Met Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala	
80 85 90	
gcc tcc ccc aac cat tcc cag ctg ctg gct tgt ggc ccc acc gtg cat	340
Ala Ser Pro Asn His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His	
95 100 105	
aga gcc tgc ggg gag gac gtg tac gcc cag ggt ttc tgt gtg ctg ctg	388
Arg Ala Cys Gly Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu	
110 115 120	
gat gcc cac gca cag ccc atc ggg act gtg cca gct gcc ctg ccc gag	436
Asp Ala His Ala Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu	
125 130 135 140	
tgc cca gat caa gag atg gac att gtc ttc ctg att gac ggc tct ggc	484
Cys Pro Asp Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly	
145 150 155	
agc att agc tca aat gac ttc cgc aag atg aag gac ttt gtc aga gct	532
Ser Ile Ser Ser Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala	
160 165 170	
gtg atg gac cag ttc aag gac acc aac acc cag ttc tcg ctg atg cag	580
Val Met Asp Gln Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln	
175 180 185	
tac tcc aat gtg ctg gtg aca cat ttc acc ttc agc agc ttc cgg aac	628
Tyr Ser Asn Val Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn	
190 195 200	
agc tcc aat cct cag ggc cta gtg gag ccc att gtg cag ctg aca ggc	676
Ser Ser Asn Pro Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly	
205 210 215 220	
ctc acg ttc acg gcc aca ggg atc ctg aaa gtg gtg aca gag ctg ttt	724
Leu Thr Phe Thr Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe	
225 230 235	
caa acc aag aac ggg gcc cgc gaa agt gcc aag aag atc ctc atc gtc	772
Gln Thr Lys Asn Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val	
240 245 250	

atc aca gat ggg cag aag tac aaa gac ccc ctg cac tac agt gct gtc Ile Thr Asp Gly Gln Lys Tyr Lys Asp Pro Leu His Tyr Ser Ala Val	820
255 260 265	
atc cca cag gca gag cag gcg ggc atc atc cgc tac gcc atc ggg gtg Ile Pro Gln Ala Glu Gln Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val	868
270 275 280	
ggg gac gcg ttc cag aaa ccc aca gcc agg cag gag ctg gac acc atc Gly Asp Ala Phe Gln Lys Pro Thr Ala Arg Gln Glu Leu Asp Thr Ile	916
285 290 295 300	
gcc tcc gag ccg ccc gac gcc cac gtg ttc cag gtg gac aat ttc tca Ala Ser Glu Pro Pro Asp Ala His Val Phe Gln Val Asp Asn Phe Ser	964
305 310 315	
gca ctc agc agc atc caa aag cag ctg tat gac agg atc ttt gcc gtc Ala Leu Ser Ser Ile Gln Lys Gln Leu Tyr Asp Arg Ile Phe Ala Val	1012
320 325 330	
gag gga acc ctg tca tcg gca agc acc tcc ttc cag cat gag atg tcc Glu Gly Thr Leu Ser Ser Ala Ser Thr Ser Phe Gln His Glu Met Ser	1060
335 340 345	
caa gag ggc ttc agc tca ctt ctc acc acg gaa gga ccg gtg ctg ggg Gln Glu Gly Phe Ser Ser Leu Leu Thr Thr Glu Gly Pro Val Leu Gly	1108
350 355 360	
gct gtg ggc agc ttc gat tgg tcc ggg ggt gct ttc ctg tac ccc ccc Ala Val Gly Ser Phe Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro	1156
365 370 375 380	
ggc ggg agc ccc acc ttc atc aac atg tct cag cag aac gtg gac atg Gly Gly Ser Pro Thr Phe Ile Asn Met Ser Gln Gln Asn Val Asp Met	1204
385 390 395	
agg gac tcc tac ctg ggt gag gaa ggg gtg ggg gtg ggg aca ggt ggg Arg Asp Ser Tyr Leu Gly Glu Glu Gly Val Gly Val Gly Thr Gly Gly	1252
400 405 410	
agc tgaggcttgg ggtggggctgg ggctgggctg ggaggggagg gaagaggagg Ser	1305
ggagaggcaa aga	1318
<210> 101	
<211> 413	
<212> PRT	
<213> rabbit	
<400> 101	
Gly Ala Val Val Leu Leu Gly Val Leu Ala Ser Tyr His Gly Phe Asn	15
1 5 10 15	
Leu Asp Val Asp Glu Pro Val Ile Phe Gln Glu Asp Ala Ala Gly Phe	30
20 25	
Gly Gln Ser Val Met Gln Phe Gly Gly Ser Arg Leu Val Val Gly Ala	45
35 40	

Pro Leu Ala Val Val Ser Ala Asn His Thr Gly Arg Leu Tyr Glu Cys
50 55 60

Ala Pro Ala Ser Gly Thr Cys Thr Pro Ile Phe Pro Phe Met Pro Pro
65 70 75 80

Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu Ala Ala Ser Pro Asn
85 90 95

His Ser Gln Leu Leu Ala Cys Gly Pro Thr Val His Arg Ala Cys Gly
100 105 110

Glu Asp Val Tyr Ala Gln Gly Phe Cys Val Leu Leu Asp Ala His Ala
115 120 125

Gln Pro Ile Gly Thr Val Pro Ala Ala Leu Pro Glu Cys Pro Asp Gln
130 135 140

Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser Ile Ser Ser
145 150 155 160

Asn Asp Phe Arg Lys Met Lys Asp Phe Val Arg Ala Val Met Asp Gln
165 170 175

Phe Lys Asp Thr Asn Thr Gln Phe Ser Leu Met Gln Tyr Ser Asn Val
180 185 190

Leu Val Thr His Phe Thr Phe Ser Ser Phe Arg Asn Ser Ser Asn Pro
195 200 205

Gln Gly Leu Val Glu Pro Ile Val Gln Leu Thr Gly Leu Thr Phe Thr
210 215 220

Ala Thr Gly Ile Leu Lys Val Val Thr Glu Leu Phe Gln Thr Lys Asn
225 230 235 240

Gly Ala Arg Glu Ser Ala Lys Lys Ile Leu Ile Val Ile Thr Asp Gly
245 250 255

Gln Lys Tyr Lys Asp Pro Leu His Tyr Ser Ala Val Ile Pro Gln Ala
260 265 270

Glu Gln Ala Gly Ile Ile Arg Tyr Ala Ile Gly Val Gly Asp Ala Phe
275 280 285

Gln Lys Pro Thr Ala Arg Gln Glu Leu Asp Thr Ile Ala Ser Glu Pro
290 295 300

Pro Asp Ala His Val Phe Gln Val Asp Asn Phe Ser Ala Leu Ser Ser
305 310 315 320

Ile Gln Lys Gln Leu Tyr Asp Arg Ile Phe Ala Val Glu Gly Thr Leu
325 330 335

Ser Ser Ala Ser Thr Ser Phe Gln His Glu Met Ser Gln Glu Gly Phe
340 345 350

Ser Ser Leu Leu Thr Thr Glu Gly Pro Val Leu Gly Ala Val Gly Ser
355 360 365

Phe Asp Trp Ser Gly Gly Ala Phe Leu Tyr Pro Pro Gly Gly Ser Pro
370 375 380

Thr Phe Ile Asn Met Ser Gln Gln Asn Val Asp Met Arg Asp Ser Tyr
385 390 395 400

Leu Gly Glu Glu Gly Val Gly Val Gly Thr Gly Gly Ser
405 410

<210> 102
<211> 1484
<212> DNA
<213> rabbit

<220>
<221> CDS
<222> (1)..(1482)

<400> 102

gat gtc cag agc tcc atc agc tat gat ctg gca ctg gac cca ggc cgc 48
Asp Val Gln Ser Ser Ile Ser Tyr Asp Leu Ala Leu Asp Pro Gly Arg
1 5 10 15

ctg gtc tct cgg gcc att ttt caa gag acc cag aac cag act tta act 96
Leu Val Ser Arg Ala Ile Phe Gln Glu Thr Gln Asn Gln Thr Leu Thr
20 25 30

cga agg aag acc ctg ggg ctg ggg cgt cac tgt gaa acc atg agg cta 144
Arg Arg Lys Thr Leu Gly Leu Gly Arg His Cys Glu Thr Met Arg Leu
35 40 45

ctt ttg cca gac tgc gta gag gac gtg gtg aac ccc atc gtc ctg cac 192
Leu Leu Pro Asp Cys Val Glu Asp Val Val Asn Pro Ile Val Leu His
50 55 60

ctc aac ttc tcc ctg gag gga cag cca atc ctc tca tcc cag aat ctg 240
Leu Asn Phe Ser Leu Glu Gly Gln Pro Ile Leu Ser Ser Gln Asn Leu
65 70 75 80

cgc cct gtg ctg gcc acg ggc tcg cag gac cac ttc att gcc tcc ctc 288
Arg Pro Val Leu Ala Thr Gly Ser Gln Asp His Phe Ile Ala Ser Leu
85 90 95

ccc ttt gag aag aac tgc gga caa gat cgc ctg tgt gag ggg gac ctg 336
Pro Phe Glu Lys Asn Cys Gly Gln Asp Arg Leu Cys Glu Gly Asp Leu
100 105 110

agc atc agc ttc aac ttc tcg ggc ttg aat acc ctg ctg gtg ggg ctc 384
Ser Ile Ser Phe Asn Phe Ser Gly Leu Asn Thr Leu Leu Val Gly Leu
115 120 125

tcc ctg gag ctc aca gtg aca gtg acc gtg cgg aat gag ggc gag gac 432
Ser Leu Glu Leu Thr Val Thr Val Arg Asn Glu Gly Glu Asp
130 135 140

tcc tat ggg acc gcc atc acc ctc tac tac cca gca ggg cta tcc tac 480
Ser Tyr Gly Thr Ala Ile Thr Leu Tyr Tyr Pro Ala Gly Leu Ser Tyr
145 150 155 160

agg cgg gtg tcg ggc cag aca caa ccc tgg cag cgc ccc ctg cac ctc 528
Arg Arg Val Ser Gly Gln Thr Gln Pro Trp Gln Arg Pro Leu His Leu
165 170 175

gca tgt gag gct gta cct acc gag agc gag ggc ttg agg agt acc acc agc Ala Cys Glu Ala Val Pro Thr Glu Ser Glu Gly Leu Arg Ser Thr Ser 180 185 190	576
tgc agc gtc aac cac ccc atc ttc caa ggg ggt gct cag ggc act ttc Cys Ser Val Asn His Pro Ile Phe Gln Gly Ala Gln Gly Thr Phe 195 200 205	624
gta gtc aag ttc gat gtc tcc tcc aag gcc agc ctg ggt gac agg ttg Val Val Lys Phe Asp Val Ser Ser Lys Ala Ser Leu Gly Asp Arg Leu 210 215 220	672
ctc atg ggg gcc agt gcc agc agt gag aat aat aag cct gcg agc aac Leu Met Gly Ala Ser Ala Ser Ser Glu Asn Asn Lys Pro Ala Ser Asn 225 230 235 240	720
aag acc tcc ttt gag ctg gaa ctg cca gtg aaa tac gct gtc tac atg Lys Thr Ser Phe Glu Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met 245 250 255	768
atg atc aca agg cac gaa ggc tcc acc agg ttc ttc aac ttt tcc act Met Ile Thr Arg His Glu Gly Ser Thr Arg Phe Phe Asn Phe Ser Thr 260 265 270	816
tcc gct gag aag agc agc aaa gag gcc gag cac cgc tat cgg gtg aac Ser Ala Glu Lys Ser Ser Lys Glu Ala Glu His Arg Tyr Arg Val Asn 275 280 285	864
aac ctg agt ctg cga gat gtg gcc gtc agc gtg gac ttc tgg gcc ccc Asn Leu Ser Leu Arg Asp Val Ala Val Ser Val Asp Phe Trp Ala Pro 290 295 300	912
gtg cag ctg aac gga gca gct gtg tgg gac gtg gcg gtg gag gcc cct Val Gln Leu Asn Gly Ala Ala Val Trp Asp Val Ala Val Glu Ala Pro 305 310 315 320	960
gcc cag agc ctg ccc tgt gcg cgg gag agg gaa cct ccg agg acc tct Ala Gln Ser Leu Pro Cys Ala Arg Glu Arg Glu Pro Pro Arg Thr Ser 325 330 335	1008
gac ctg agc cgg gtc ccg ggg agt ccc gtg ctg gac tgc agc gtt gcg Asp Leu Ser Arg Val Pro Gly Ser Pro Val Leu Asp Cys Ser Val Ala 340 345 350	1056
cac tgc ctg agg ttc cgc tgc cac atc ccc tcc ttc agc gcc aag gag His Cys Leu Arg Phe Arg Cys His Ile Pro Ser Phe Ser Ala Lys Glu 355 360 365	1104
gag ctc cac ttc acc ctg aag ggc aac ctc agc ttc gcc tgg gtc agc Glu Leu His Phe Thr Leu Lys Gly Asn Leu Ser Phe Ala Trp Val Ser 370 375 380	1152
cag atg ctg caa aag aag gtg tcg gtg agt gtg gcc gag atc acc Gln Met Leu Gln Lys Lys Val Ser Val Val Ser Val Ala Glu Ile Thr 385 390 395 400	1200
ttc aac agg gcc gtg tac tcc caa gtt ccg ggc gag gag ccc ttt atg Phe Asn Arg Ala Val Tyr Ser Gln Val Pro Gly Glu Glu Pro Phe Met 405 410 415	1248

aga gcc cag gtg gag acg gtg ctg gag gag tat gag gag cac gac ccc	1296		
Arg Ala Gln Val Glu Thr Val Leu Glu Glu Tyr Glu Glu His Asp Pro			
420	425	430	
gtc ccc ctg gtg gtc ggc agc tgt gtg ggc ggc ctg ctg ctg ctg gct	1344		
Val Pro Leu Val Val Gly Ser Cys Val Gly Gly Leu Leu Leu Ala			
435	440	445	
ctc atc tca gcc acc ctg tac aag ctt ggc ttc ttc aag cgc cg ^g tac	1392		
Leu Ile Ser Ala Thr Leu Tyr Lys Leu Gly Phe Phe Lys Arg Arg Tyr			
450	455	460	
aag gag atg ctg ggc gag aaa ccg gga gac gcg gcc acc ttc ccc ggg	1440		
Lys Glu Met Leu Gly Glu Lys Pro Gly Asp Ala Ala Thr Phe Pro Gly			
465	470	475	480
gag gac gcc agc tgc ggg gct tca gat ttg cct ttg tcc cag tg	1484		
Glu Asp Ala Ser Cys Gly Ala Ser Asp Leu Pro Leu Ser Gln			
485	490		

<210> 103

<211> 494

<212> PRT

<213> rabbit

<400> 103

Asp Val Gln Ser Ser Ile Ser Tyr Asp Leu Ala Leu Asp Pro Gly Arg

1

5

10

15

Leu Val Ser Arg Ala Ile Phe Gln Glu Thr Gln Asn Gln Thr Leu Thr

20

25

30

Arg Arg Lys Thr Leu Gly Leu Gly Arg His Cys Glu Thr Met Arg Leu

35

40

45

Leu Leu Pro Asp Cys Val Glu Asp Val Val Asn Pro Ile Val Leu His

50

55

60

Leu Asn Phe Ser Leu Glu Gly Gln Pro Ile Leu Ser Ser Gln Asn Leu

65

70

75

80

Arg Pro Val Leu Ala Thr Gly Ser Gln Asp His Phe Ile Ala Ser Leu

85

90

95

Pro Phe Glu Lys Asn Cys Gly Gln Asp Arg Leu Cys Glu Gly Asp Leu

100

105

110

Ser Ile Ser Phe Asn Phe Ser Gly Leu Asn Thr Leu Leu Val Gly Leu

115

120

125

Ser Leu Glu Leu Thr Val Thr Val Arg Asn Glu Gly Glu Asp

130

135

140

Ser Tyr Gly Thr Ala Ile Thr Leu Tyr Tyr Pro Ala Gly Leu Ser Tyr

145

150

155

160

Arg Arg Val Ser Gly Gln Thr Gln Pro Trp Gln Arg Pro Leu His Leu

165

170

175

Ala Cys Glu Ala Val Pro Thr Glu Ser Glu Gly Leu Arg Ser Thr Ser
180 185 190

Cys Ser Val Asn His Pro Ile Phe Gln Gly Gly Ala Gln Gly Thr Phe
195 200 205

Val Val Lys Phe Asp Val Ser Ser Lys Ala Ser Leu Gly Asp Arg Leu
210 215 220

Leu Met Gly Ala Ser Ala Ser Ser Glu Asn Asn Lys Pro Ala Ser Asn
225 230 235 240

Lys Thr Ser Phe Glu Leu Glu Leu Pro Val Lys Tyr Ala Val Tyr Met
245 250 255

Met Ile Thr Arg His Glu Gly Ser Thr Arg Phe Phe Asn Phe Ser Thr
260 265 270

Ser Ala Glu Lys Ser Ser Lys Glu Ala Glu His Arg Tyr Arg Val Asn
275 280 285

Asn Leu Ser Leu Arg Asp Val Ala Val Ser Val Asp Phe Trp Ala Pro
290 295 300

Val Gln Leu Asn Gly Ala Ala Val Trp Asp Val Ala Val Glu Ala Pro
305 310 315 320

Ala Gln Ser Leu Pro Cys Ala Arg Glu Arg Glu Pro Pro Arg Thr Ser
325 330 335

Asp Leu Ser Arg Val Pro Gly Ser Pro Val Leu Asp Cys Ser Val Ala
340 345 350

His Cys Leu Arg Phe Arg Cys His Ile Pro Ser Phe Ser Ala Lys Glu
355 360 365

Glu Leu His Phe Thr Leu Lys Gly Asn Leu Ser Phe Ala Trp Val Ser
370 375 380

Gln Met Leu Gln Lys Lys Val Ser Val Val Ser Val Ala Glu Ile Thr
385 390 395 400

Phe Asn Arg Ala Val Tyr Ser Gln Val Pro Gly Glu Glu Pro Phe Met
405 410 415

Arg Ala Gln Val Glu Thr Val Leu Glu Glu Tyr Glu Glu His Asp Pro
420 425 430

Val Pro Leu Val Val Gly Ser Cys Val Gly Gly Leu Leu Leu Ala
435 440 445

Leu Ile Ser Ala Thr Leu Tyr Lys Leu Gly Phe Phe Lys Arg Arg Tyr
450 455 460

Lys Glu Met Leu Gly Glu Lys Pro Gly Asp Ala Ala Thr Phe Pro Gly
465 470 475 480

Glu Asp Ala Ser Cys Gly Ala Ser Asp Leu Pro Leu Ser Gln
485 490

<210> 104
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 104
tgtccaggac aagagatgga cattgc

26

<210> 105
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 105
gagcttatttc atagcaagaa tggg

24

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 106
tatagcatag cgaatgtatcc

20

<210> 107
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 107
atggtccgtg gagttgtat c

21

<210> 108
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 108
tcgagatcca ccaaactgca c

21

<210> 109
<211> 14

<212> PRT
<213> monkey

<400> 109
Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala
1 5 10

<210> 110
<211> 14
<212> PRT
<213> monkey

<400> 110
Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Xaa Glu Asp Ala
1 5 10

<210> 111
<211> 15
<212> PRT
<213> monkey

<400> 111
Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala
1 5 10 15

<210> 112
<211> 17
<212> PRT
<213> Homo sapiens

<400> 112
Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala Gly
1 5 10 15
Gly

<210> 113
<211> 16
<212> PRT
<213> Homo sapiens

<400> 113
Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Val Asp Ser Ala Gly
1 5 10 15

<210> 114
<211> 17
<212> PRT
<213> Homo sapiens

<400> 114
Phe Asn Leu Asp Thr Glu Asn Ala Met Thr Phe Gln Glu Asn Ala Arg
1 5 10 15
Gly